

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 17:04:25 ; Search time 15.1307 Seconds
(without alignments)
1593.347 Million cell updates/sec

Title: US-10-037-860-13

Perfect score: 2423

Sequence: 1 MPTLLQDWCRGHEHLNTRC.....VESGNGNWAWDKSHPKSKAK 463

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	836.5	34.5	364	1 PMA2 HUMAN	Q9u42 homo sapien
2	826.5	34.1	364	1 PMA2 MACFA	Q9gm3 macaca fasc
3	822	33.9	353	1 PMA1 MOUSE	Q8cl8 mus musculus
4	822	33.9	353	1 PMA1 RAT	Q8vz4 rattus norv
5	818	33.8	353	1 PMA1 HUMAN	Q8nd90 homo sapien
6	768.5	31.7	351	1 MOP1 HUMAN	Q96by2 homo sapien
7	761.5	31.4	351	1 MOP1 MACFA	Q95ki4 macaca fasc
8	725.5	29.9	365	1 PMA2 MOUSE	Q8bhk0 mus musculus
9	711	29.3	352	1 MOP1 MOUSE	Q8erb6 mus musculus
10	114.5	4.7	474	1 LAM3 MOUSE	P48680 mus musculus
11	113	4.7	476	1 ENGA RHINE	Q92uk6 rhizobium m
12	113	4.7	3674	1 SPCR HUMAN	Q9nrc6 homo sapien
13	110	4.5	373	1 CK13 HUMAN	Q02833 homo sapien
14	107.5	4.4	817	1 PERQ HUMAN	O75420 homo sapien
15	106.5	4.4	301	1 SSB DEIRA	O9ry51 deinococcus
16	106.5	4.4	857	1 MED6 GIALA	Q88014 giardia lam
17	105.5	4.4	813	1 TTDA DROME	P42282 trophoblast
18	105	4.3	783	1 RIN1 HUMAN	Q13671 homo sapien
19	105	4.3	804	1 SYM ORYSA	Q9zts1 oryza sativ
20	105	4.3	4625	1 DYIA CHLRE	Q9smh3 chlamydomon
21	104.5	4.3	864	1 PAVO SULSO	O97wh0 sulfolobus
22	104	4.3	483	1 ENGA BRUME	Q8yfh2 brucella me
23	104	4.3	483	1 ENGA BRUSU	Q9gze8 brucella su
24	104	4.3	2564	1 SPCQ HUMAN	Q9h254 homo sapien
25	103	4.3	860	1 IF2 RHIL0	Q98bi8 rhizobium l
26	103	4.3	1011	1 PERQ MOUSE	Q99mr1 mus musculus
27	102.5	4.2	4367	1 DYHC NEUCR	P45443 neurospora
28	101.5	4.2	1733	1 VNDA PRVKA	P33485 pseudorabie
29	100	4.1	384	1 AIPL HUMAN	Q9nzn9 homo sapien
30	100	4.1	384	1 AIPL PANPA	Q95mn9 pan paniscu
31	99.5	4.1	600	1 LAM2 CHICK	P14732 gallus gall
32	99.5	4.1	1050	1 BULB HUMAN	O60566 homo sapien
33	99	4.1	398	1 MPK2_CHICK	Q90891 gallus gall

34 98.5 4.1 692 1 MYS PODCA
35 98.5 4.1 1197 1 CING_HUMAN
36 98.5 4.1 3680 1 DMD_CANFA
37 98 4.0 1268 1 YRD6 CAEEL
38 97.5 4.0 476 1 ENGA AGRT5
39 97.5 4.0 888 1 M3KC RAT
40 97.5 4.0 1178 1 DSRA_MOUSE
41 97 4.0 524 1 EXP9_STRPN
42 97 4.0 780 1 CUL5_RABIT
43 96.5 4.0 441 1 GAG_CAEVC
44 96.5 4.0 570 1 SYG_ARCFU
45 96.5 4.0 714 1 CLPB_MYCGE

ALIGNMENTS

RESULT 1
PMA2 HUMAN
ID PMA2_HUMAN STANDARD; PRT; 364 AA.
AC Q9UL42; Q94959; Q95145; Q9UL43;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Paraneoplastic antigen Ma2 (Onconeural antigen MA2) (Paraneoplastic
DB neuronal antigen MM2) (40 kDa neuronal protein).
GN PMA2 OR MA2 OR KIA0883.
OS Homo sapiens (Human).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Cerebellum;
RX MEDLINE=99270611; PubMed=10362822;
RA Voltz R., Gultekin S.H., Rosenfeld M.R., Gerstner E., Eichen J.,
RA Posner J.B., Dalmay J.;
RT "A serologic marker of paraneoplastic limbic and brain-stem
encephalitis in patients with testicular cancer.";
RL New Engl. J. Med. 340:1788-1795(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
RL DNA Res. 5:355-364(1998).
RN [3]
RP IDENTIFICATION, AND SUBCELLULAR LOCATION.
RX MEDLINE=99158179; PubMed=10050892;
RA Dalmay J., Gultekin S.H., Voltz R., Hoard R., DesChamps T.,
RA Balmaceda C., Batchelor T., Gerstner E., Eichen J., Frennier J.,
RA Posner J.B., Rosenfeld M.R.;
RT "Ma1, a novel neuron- and testis-specific protein, is recognized by
the serum of patients with paraneoplastic neurological disorders.";
RL Brain 122:27-39(1999).
RN [4]
RP SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -!- TISSUE SPECIFICITY: Brain specific. In some patients suffering
from cancers, it is also specifically expressed by the testicular
tumor cells.
CC -!- MISCELLANEOUS: Antibodies against PMA2 are present in sera from
patients suffering of paraneoplastic neurological disorders.
CC -!- SIMILARITY: Belongs to the PMA family.

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CC EMBL; AF037365; AD02098.1; -
CC EMBL; AF083114; AAF05625.1; -
CC EMBL; AF083115; AAF05626.1; -
CC EMBL; AF286487; AAG28165.1; -
CC EMBL; AB020690; BAA74906.1; -
CC Genew; HGNC:9159; PNMA2.
CC MIM; 603970; -.
KW Antigen; Tumor antigen; Nuclear protein.
FT DOMAIN 333 338 POLY-GLU.
FT CONFLICT 128 129 GV -> AL (IN REF. 1; AAD02098).
FT CONFLICT 141 141 LV -> I (IN REF. 1; AAD02098).
FT CONFLICT 257 257 T -> P (IN REF. 1; AAF05625).
FT CONFLICT 278 278 R -> K (IN REF. 1; AAF05626).
SQ SEQUENCE 364 AA; 41509 MW; 6E417AD96E3F0593 CRC64;

Query Match 34.5%; Score 836.5; DB 1; Length 364;
Best Local Similarity 49.7%; Pred. No. 2.4e-53;
Matches 174; Conservative 63; Mismatches 108; Indels 5; Gaps 3;

QY 1 MPTLLQDWCRCGHEHLNTRCMLILGIPEDCGEDEFETLQEAACHLGRYRVIGRMFRREE 60
DB 1 MALALLEDCRIMSVDQKSLMVTGIPVDYEEAEIQEVLTQKSLGRLKGIKFRKQE 60
QY 61 NQAAILLEAODIDYALLPREIPGKGPWEIVVKPNSDGEFLNRLNRLFEERRTVSDM 120
DB 61 NANAVLLELLEDDTDSVAISEVQGGKGVKVPKTPNQDTEFLERLNLFLEKRGQTVSGM 120
QY 121 NRVLSGSDTNCSPRVITISPEFWT--WAQTILGAAVQPLLEQMLYRELRFVSGNTISIPGAL 178
DB 121 FRALQEGVSPATVPICISPELLAHLGQAMAHAPQLL-PMRYKLRVFGSVAVPAPEE 179
QY 179 AFDAMLEHTTEMLQMWQVPEGEKRRRLMECLRGPALQVGVGLRASNASTVEECLAAQQ 238
DB 180 SPEVWLEQATEIVKVPVTEAEKKRWLAESLRGPDALDLMHIVQADNPISVEECLFAFKQ 239
QY 239 VFGPVESHKIAOVKLCAYOEAGEKVSFVLRLPELLOQAVENNVSRNVNQLKRVL 298
DB 240 VFGSLESRTAQVRYLKYQEAGEKVSAYVLRLETLRRRAVEKRAIPRIADQVRLEQVM 299
QY 299 SGATLPDKLRDKLQMKQRKPPGFALVKLRLREEEWEATLGPDRRESLE 348
DB 300 AGATLNQMLWCLRELKQDGGPPSFLELMKVIREEEBEASFP--ENESIE 347

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RESULT 2

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PMA2 MACFA STANDARD; PRT; 364 AA.
AC Q9GMU3;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Paraneoplastic antigen Mac2 homolog.
GN PNMA2.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
CC -!- SIMILARITY: Belongs to the PNMA family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; AB047632; BAB12156.1; -.
CC Nuclear protein.
FT DOMAIN 333 338 POLY-GLU.
FT SEQUENCE 364 AA; 41350 MW; 0CF72210D7EC1524 CRC64;

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Query Match 34.1%; Score 826.5; DB 1; Length 364;
Best Local Similarity 49.1%; Pred. No. 1.3e-52;
Matches 172; Conservative 63; Mismatches 110; Indels 5; Gaps 3;

QY 1 MPTLLQDWCRCGHEHLNTRCMLILGIPEDCGEDEFETLQEAACHLGRYRVIGRMFRREE 60
DB 1 MALALLEDCRIMSVDQKSLMVTGIPVDYEEAEIQEVLTQKSLGRLKGIKFRKQE 60
QY 61 NQAAILLEAODIDYALLPREIPGKGPWEIVVKPNSDGEFLNRLNRLFEERRTVSDM 120
DB 61 NANAVLLELLEDDTDSVAISEVQGGKGVKVPKTPNQDTEFLERLNLFLEKRGQTVSGM 120
QY 121 NRVLSGSDTNCSPRVITISPEFWT--WAQTILGAAVQPLLEQMLYRELRFVSGNTISIPGAL 178
DB 121 FRALQEGVSPATVPICISPELLAHLGQAMAHAPQLL-PMRYKLRVFGSVAVPAPEE 179
QY 179 AFDAMLEHTTEMLQMWQVPEGEKRRRLMECLRGPALQVGVGLRASNASTVEECLAAQQ 238
DB 180 SPEVWLEQATEIVKVPVTEAEKKRWLAESLRGPDALDLMHIVQADNPISVEECLFAFKQ 239
QY 239 VFGPVESHKIAOVKLCAYOEAGEKVSFVLRLPELLOQAVENNVSRNVNQLKRVL 298
DB 240 VFGSLESRTAQVRYLKYQEAGEKVSAYVLRLETLRRRAVEKRAIPRIADQVRLEQVM 299
QY 299 SGATLPDKLRDKLQMKQRKPPGFALVKLRLREEEWEATLGPDRRESLE 348
DB 300 AGATLNQMLWCLRELKQDGGPPSFLELMKVIREEEBEASFP--ENESIE 347

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RESULT 3

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PMA1 MOUSE STANDARD; PRT; 353 AA.
ID PM1 MOUSE
AC O8CJG8; O9CVP2;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Paraneoplastic antigen Mal homolog.
GN PNMA1 OR MA1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain, and Embryo;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Shriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reid D.J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,

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RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
CC -|- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
CC -|- SIMILARITY: Belongs to the PNMA family.
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CC -----
DR EMBL; AK017476; BAB30762.1; -.
DR EMBL; AK028331; BAC25885.1; -.
DR MGD; MGI:2180564; Pnma1.
KW Nuclear protein.
FT DOMAIN 336 341 POLY-GLU.
FT CONFLICT 136 136 T->M (IN REF. 1; BAB30762).
SQ SEQUENCE 353 AA; 39688 MW; 18CEDC3AC4E70939 CRC64;

Query Match 33.9%; Score 822; DB 1; Length 353;
Best Local Similarity 49.4%; Pred. No. 2.6e-52;
Matches 175; Conservative 54; Mismatches 117; Indels 8; Gaps 4;

Qy 1 MPTLLQDWCGRGHEHNTTRCMLILGIPDCGDEFEETLQEAACHLGRYRVIQGMFRREE 60
Db 1 MAMTLLDWCGRGDMVNSQRALLVWGIPVNCDETIETLQAMPQVS-YRVLGRMFWRREE 59

Qy 61 NQAAILLEAQDIDYALLPREIPGKGGPWEVIVPRNSDGEFFLNRLNRFLEERRTVSDM 120
Db 60 NAKAALLELTGVDVSYLIPREMPGKGLKVKVPPTSDAFLERLHLFLAREGWTQDV 119

Qy 121 NRVLGSDNTCSAPRTVISPEFTWQAOTLGAQVQLPQLMQLYRELRVFSNGTISIPGALAF 180
Db 120 ARVLGFQNPAPAPGPETPAEMLN--ILDNVIQPLVESIWKLTLSFGDKDIPGGEETF 177

Qy 181 DAWLEHTTEMLQWQVPEGEKRRRLMECLRGPAQVQVSGLRASNASITVEECLAQOVF 240
Db 178 DSWLEHSENEIIEWQVSDIEKRRRLMSLRGPAADVIRILKTNNAITTAELKALEQVF 237

Qy 241 GPVESHKIAQVKLCAYQEAQEKVSSFFVLRLEPLLQRAVENNVVSRNNVTRLRKRVLSG 300
Db 238 GSVESSRDAQVRFLNTYQNPGEKLSYVIRLEPLLQKVDKGVIDKONVNQARLEQVIAG 297

Qy 301 ATLPDKLRDKLQKMKQRKP-PGFLALVKLLRE-----EEWEATLGPDRSLEG 349
Db 298 ANHSGALRRQLWLAGAGPGAPNLFQLLVQIREBEAKKEEAEAAALQLGLEG 351

RESULT 4
PMAL RAT STANDARD; PRT; 353 AA.
ID PMAL RAT
AC Q8VHZ4;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Paraneoplastic antigen Mal homolog.
GN PNMA1 OR MAL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
CC -|- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
CC -|- SIMILARITY: Belongs to the PNMA family.
CC -----
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CC -----
DR EMBL; AK017476; BAB30762.1; -.
DR EMBL; AK028331; BAC25885.1; -.
DR MGD; MGI:2180564; Pnma1.
KW Nuclear protein.
FT DOMAIN 336 341 POLY-GLU.
FT CONFLICT 136 136 T->M (IN REF. 1; BAB30762).
SQ SEQUENCE 353 AA; 39688 MW; 18CEDC3AC4E70939 CRC64;

Query Match 33.9%; Score 822; DB 1; Length 353;
Best Local Similarity 49.4%; Pred. No. 2.6e-52;
Matches 175; Conservative 54; Mismatches 117; Indels 8; Gaps 4;

Qy 1 MPTLLQDWCGRGHEHNTTRCMLILGIPDCGDEFEETLQEAACHLGRYRVIQGMFRREE 60
Db 1 MAMTLLDWCGRGDMVNSQRALLVWGIPVNCDETIETLQAMPQVS-YRVLGRMFWRREE 59

Qy 61 NQAAILLEAQDIDYALLPREIPGKGGPWEVIVPRNSDGEFFLNRLNRFLEERRTVSDM 120
Db 60 NAKAALLELTGVDVSYLIPREMPGKGLKVKVPPTSDAFLERLHLFLAREGWTQDV 119

Qy 121 NRVLGSDNTCSAPRTVISPEFTWQAOTLGAQVQLPQLMQLYRELRVFSNGTISIPGALAF 180
Db 120 ARVLGFQNPAPAPGPETPAEMLN--ILDNVIQPLVESIWKLTLSFGDKDIPGGEETF 177

Qy 181 DAWLEHTTEMLQWQVPEGEKRRRLMECLRGPAQVQVSGLRASNASITVEECLAQOVF 240
Db 178 DSWLEHSENEIIEWQVSDIEKRRRLMSLRGPAADVIRILKTNNAITTAELKALEQVF 237

Qy 241 GPVESHKIAQVKLCAYQEAQEKVSSFFVLRLEPLLQRAVENNVVSRNNVTRLRKRVLSG 300
Db 238 GSVESSRDAQVRFLNTYQNPGEKLSYVIRLEPLLQKVDKGVIDKONVNQARLEQVIAG 297

Qy 301 ATLPDKLRDKLQKMKQRKP-PGFLALVKLLRE-----EEWEATLGPDRSLEG 349
Db 298 ANHSGALRRQLWLAGAGPGAPNLFQLLVQIREBEAKKEEAEAAALQLGLEG 351

RESULT 5
PMAL HUMAN STANDARD; PRT; 353 AA.
ID PMAL HUMAN
AC Q8ND90; Q95144; Q8NG07;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Paraneoplastic antigen Mal (Neuron- and testis-specific protein 1)
DE (37 kDa neuronal protein).
GN PNMA1 OR MAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Cerebellum;

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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=99158179; PubMed=10050892;
RA Dalmat J., Gultekin S.H., Voltz R., Hoard R., DesChamps T.,
RA Balmaceda C., Batchelor T., Gerstner E., Bichen J., Frenn J.,
RA Posner J.B., Rosenfeld M.R.;
RT "Mal, a novel neuron- and testis-specific protein, is recognized by
RT the serum of patients with paraneoplastic neurological disorders.";
RL Brain 122:27-39 (1999).
CC -|- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
CC -|- TISSUE SPECIFICITY: Testis and brain specific.
CC -|- SIMILARITY: Belongs to the PNMA family.
CC -----
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CC -----
DR EMBL; AF335505; AAL73196.1; -.
DR EMBL; AF335505; AAL73196.1; -.
KW Nuclear protein.
FT DOMAIN 335 341 POLY-GLU.
FT CONFLICT 335 335 T->M (IN REF. 1; BAB30762).
SQ SEQUENCE 353 AA; 39793 MW; FFC3A717FDCEADA3 CRC64;

Query Match 33.9%; Score 822; DB 1; Length 353;
Best Local Similarity 49.2%; Pred. No. 2.6e-52;
Matches 174; Conservative 55; Mismatches 117; Indels 8; Gaps 4;

Qy 1 MPTLLQDWCGRGHEHNTTRCMLILGIPDCGDEFEETLQEAACHLGRYRVIQGMFRREE 60
Db 1 MAMTLLDWCGRGDMVNSQRALLVWGIPVNCDETIETLQAMPQVS-YRVLGRMFWRREE 59

Qy 61 NQAAILLEAQDIDYALLPREIPGKGGPWEVIVPRNSDGEFFLNRLNRFLEERRTVSDM 120
Db 60 NAKAALLELTGVDVSYLIPREMPGKGLKVKVPPTSDAFLERLHLFLAREGWTQDV 119

Qy 121 NRVLGSDNTCSAPRTVISPEFTWQAOTLGAQVQLPQLMQLYRELRVFSNGTISIPGALAF 180
Db 120 ARVLGFQNPAPAPGPETPAEMLN--ILDNVIQPLVESIWKLTLSFGDKDIPGGEETF 177

Qy 181 DAWLEHTTEMLQWQVPEGEKRRRLMECLRGPAQVQVSGLRASNASITVEECLAQOVF 240
Db 178 DSWLEHSENEIIEWQVSDIEKRRRLMSLRGPAADVIRILKTNNAITTAELKALEQVF 237

Qy 241 GPVESHKIAQVKLCAYQEAQEKVSSFFVLRLEPLLQRAVENNVVSRNNVTRLRKRVLSG 300
Db 238 GSVESSRDAQVRFLNTYQNPGEKLSYVIRLEPLLQKVDKGVIDKONVNQARLEQVIAG 297

Qy 301 ATLPDKLRDKLQKMKQRKP-PGFLALVKLLRE-----EEWEATLGPDRSLEG 349
Db 298 ANHSGALRRQLWLAGAGPGAPNLFQLLVQIREBEAKKEEAEAAALQLGLEG 351

RESULT 5
PMAL HUMAN STANDARD; PRT; 353 AA.
ID PMAL HUMAN
AC Q8ND90; Q95144; Q8NG07;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Paraneoplastic antigen Mal (Neuron- and testis-specific protein 1)
DE (37 kDa neuronal protein).
GN PNMA1 OR MAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Cerebellum;

```


RA Stapleton M., Soares M.B., Ronaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McQuellan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fahney J., Heiton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalbus D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Mediates caspase-dependent apoptosis.
 CC -!- SUBUNIT: Homodimer. Binds BAX, BCL2 and BCLX.
 CC -!- TISSUE SPECIFICITY: Ubiquitously expressed with higher levels in
 CC heart and brain.
 CC -!- DOMAIN: The BH3-like domain is required for association with BAX
 CC and for mediating apoptosis. The three BH domains (BH1, BH2, and
 CC BH3) of BAX are all required for mediating protein-protein
 CC interaction.
 CC -!- SIMILARITY: Belongs to the PNMA family.
 CC -!- CAUTION: Ref.2 sequence differs from that shown due to a
 CC frameshift in position 102.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL; AF305550; AAC31786.1; -
 CC EMBL; AK024029; BAB14788.1; ALT_SEQ.
 CC EMBL; BC015044; AAH15044.1; -
 CC Genbank; HGNC:16658; MOAP1.
 CC Apoptosis.
 CC SITE 120 127 BH3-LIKE.
 CC MUTAGEN 120 127 MISSING: ABROGATED INTERACTION WITH BAX,
 CC RESULTING IN A NONAPOPTOTIC PROTEIN.
 CC MUTAGEN 120 120 L->E: WEAKENED INTERACTION WITH BAX,
 CC RESULTING IN A NONAPOPTOTIC PROTEIN.
 CC MUTAGEN 125 127 GHE->VLA: ABROGATED INTERACTION WITH BAX,
 CC RESULTING IN A NONAPOPTOTIC PROTEIN.
 CC MUTAGEN 244 244 T -> A (IN REF. 2).
 CC CONFLICT 258 258 Y -> H (IN REF. 2).
 CC CONFLICT 259 259 Q -> H (IN REF. 1).
 CC SEQUENCE 351 AA; 39512 MW; 5310142AC02B563C CRC64;
 CC
 CC Query Match 31.7%; Score 768.5; DB 1; Length 351;
 CC Best Local Similarity 46.6%; Pred. No. 1.9e-48;
 CC Matches 165; Conservative 60; Mismatches 118; Indels 11; Gaps 6;
 CC
 CC 1 MPTLLQDWCGRGHLNTRRCMLILGIPDCGDEFEFTLQACRHLGRLYRVRIGMFRREE 60
 CC 1 MTLRLLEDWCGRGMDNPRKALLIAGISQSCSVAEIEEALQAGLAPLGEYRLGLRMFRDE 60
 CC 61 NQAAILLELAQDIDYALLPREIPCKGGPWEIVVPRNSDGEFLNRLNRFLEERRTVSDM 120
 CC 61 NRKVALVGLTAEETSHALVPKEIPGKGIWVIFKPPDPDNTFLSRNLNFEFLAGEGWTGVEL 120
 CC 121 NRVLGSDTNCSPARTVISPEFWT--WAQTLGAAYVQPLLEQMLYRELVRVFSGNTISIPGAL 178
 CC 121 SRALCHENGSLDPEQGMIPENWAPMLAQAAL-EALQPALQCLKYKKLVRFSRESPEPEEE 179
 CC 179 AFDALWEHTTLMQWQVPEGEKRRRLMECLRGPALQVSGLRASNASITVEECALAQ 238
 CC 180 EFGRWMEHTTQMIKAWQVPDVEKRRRLLESIRGPDALDVRVLKINNPLITVDECIQALEE 239
 CC 239 VFGPVESHKIAQVLCCKAYQAGEKVSFVLEFLPLQLQRAVNNVSRNNVQTRLKRVL 298

DB 240 VFGVTNPRELQVYLYTYQDEKLSAYVLRLEPLQKLVQRCAGIEDAVNQALDQVI 299
 QY 299 SGATPLDKLRDKLKMQRKPPGFIALVKLRE---EEWEATLGPDRSLEG 349
 DB 300 AGA-VHKTIRRELNL-PEDGAPGFLQLLVIXDYAAEEBELL---QAILEG 348
 RESULT 7
 ID MOAP1 MACFA STANDARD; PRT; 351 AA.
 AC Q95K14;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Modulator of apoptosis 1 (MAP-1).
 GN MOAP1.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OC NCBI_TaxID=9541;
 RN NCBI_TaxID=9541;
 RN SEQUENCE FROM N.A.
 RP TISSUE-Temporal cortex;
 RC Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RA "Isolation of full-length cDNA clones from macaque brain cDNA
 RA libraries";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Mediates caspase-dependent apoptosis (By similarity).
 CC -!- SUBUNIT: Homodimer. Binds BAX, BCL2 and BCLX (By similarity).
 CC -!- DOMAIN: The BH3-like domain is required for association with BAX
 CC and for mediating apoptosis. The three BH domains (BH1, BH2, and
 CC BH3) of BAX are all required for mediating protein-protein
 CC interaction (By similarity).
 CC -!- SIMILARITY: Belongs to the PNMA family.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL; AB060854; BAB46873.1; -
 CC Apoptosis.
 CC SITE 120 127 BH3-LIKE.
 CC MUTAGEN 336 339 POLY-GLU.
 CC SEQUENCE 351 AA; 39623 MW; C7530E4496A6FFB3 CRC64;
 CC
 CC Query Match 31.4%; Score 761.5; DB 1; Length 351;
 CC Best Local Similarity 46.6%; Pred. No. 6.3e-48;
 CC Matches 165; Conservative 59; Mismatches 119; Indels 11; Gaps 6;
 CC
 CC 1 MPTLLQDWCGRGHLNTRRCMLILGIPDCGDEFEFTLQACRHLGRLYRVRIGMFRREE 60
 CC 1 MTLRLLEDWCGRGMDNPRKALLIAGISQSCSVAEIEEALQAGLAPLGEYRLGLRMFRDE 60
 CC 61 NQAAILLELAQDIDYALLPREIPCKGGPWEIVVPRNSDGEFLNRLNRFLEERRTVSDM 120
 CC 61 NRKVALVGLTAEETSHALVPKEIPGKGIWVIFKPPDPDNTFLSRNLNFEFLAGEGWTGVEL 120
 CC 121 NRVLGSDTNCSPARTVISPEFWT--WAQTLGAAYVQPLLEQMLYRELVRVFSGNTISIPGAL 178
 CC 121 SRALCHENGSLDPEQGMIPENWAPMLAQAAL-EALQPALQCLKYKKLVRFSRESPEPEEE 179
 CC 179 AFDALWEHTTLMQWQVPEGEKRRRLMECLRGPALQVSGLRASNASITVEECALAQ 238
 CC 180 EFGRWMEHTTQMIKAWQVPDVEKRRRLLESIRGPDALDVRVLKINNPLITVDECIQALEE 239
 CC 239 VFGPVESHKIAQVLCCKAYQAGEKVSFVLEFLPLQLQRAVNNVSRNNVQTRLKRVL 298

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Db 240 VEGVTNPRELQVLYTTQKDEEKLKSAVYLRLEPLLQKLVQGAERDAVQARLDQVI 299
QY 299 SGATLPDKLRLKLMQKQKPPGFLALVKLRE---EEWEATLPDRESLEG 349
Db 300 AGA-VHKTIRRELNL-PEDGPAPGFLQLLVLIKDYEAABEEALL---QEVLEG 348

RESULT 8
PMA2 MOUSE
ID PMA2 MOUSE STANDARD; PRT; 365 AA.
AC Q9BHK0;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Paraneoplastic antigen M2 homolog.
GN PMA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Brain cortex;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Knapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Redziarski R.M., King B.L.,
RA Konggaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer M., Akamatsu N., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
CC -!- SIMILARITY: Belongs to the PMA family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL AK043718; BAC31626.1; -
CC EMBL AK043910; BAC31700.1; -
CC MGD; MGI:2444129; Pma2.
CC
CC Nuclear protein.
CC
CC DOMAIN 333 338 POLY-GLU.
CC SEQUENCE 365 AA; 41201 MW; 0F90C940B9D843D9 CRC64;
CC
Query Match 29.9%; Score 725.5; DB 1; Length 365;

```

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Best Local Similarity 43.4%; Pred. No. 2.7e-45;
Matches 148; Conservative 76; Mismatches 110; Indels 7; Gaps 3;

QY 1 MPUTLLQDWCRCHELNTRCMLILGIPDCGEDEFETLQEA CRHLGRYRVIGMRFRREE 60
Db 1 MAVALLEEWCKMGVDVQKSLVVDIPVDCGEBEIQTVLQEA LKCVGSYLLGKIFQKQD 60

QY 61 NAQAIILELAQDIDYALLPREIPGKGPWEIVKPRNSDGEFLNRLNRLFEERRVSDM 120
Db 61 NTSVVLVELMDETDMSVFPSEVQGGVWKVFKPTFNQDTEFLQRLNLFLEKEGQIVAGM 120

QY 121 NRVLGSDTNCSPRVTVISPEFWTAQTLGAAV---OPLLEOMLYRELRFVSGNTTISIPG 176
Db 121 FRALKHEGVSPATPPCTSPEL--LAHLTQAMVHGQRP LL-FVKYCKMIFSGSTAAPE 177

QY 177 ALAFDAWLHETTEMLOMQVPEGEKRRRLMECLRG PALQVVGSLRASNAITVEECLAAL 236
Db 178 EEPFVWLQEATEIAKEWPIPEAEKKRWVAESLRG PALDLMHIVQADNPSISVGECLFAF 237

QY 237 QOVFGPVESHKTAOVKLCAYQEAQEKVSSFVLRLEPILQRAVENNVVRRNVNQTLLKR 296
Db 238 KOVFGSTESRRTSQVKYLRTYQOEGEKISAYVLRLEP LTLRRRAVEKRAIPNTIADQVRLEQ 297

QY 297 VLSGATLPDKLRDKLKLKMQRRKPPGFLALVKLREEEWE 337
Db 298 VVAGANLGNVLNCRLOELKDKQGLPTFLQLMKVIREEEEEE 338

RESULT 9
MOP1 MOUSE
ID MOP1 MOUSE STANDARD; PRT; 352 AA.
AC Q9ERH6;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Modulator of apoptosis 1 (MAP-1).
GN MOAP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21264738; PubMed=11060313;
RA Tan K.O., Tan K.M.L., Chan S.-L., Yee K.S.Y., Bevort M., Ang K.C.,
RA Yu V.C.;
RT "MAP-1, a novel proapoptotic protein containing a BH3-like motif that
RT associates with Bax through its Bcl-2 homology domains.";
RL J. Biol. Chem. 276:2802-2807 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Frieschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";

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RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic, and Kidney;
RX MEDLINE=22398257; PubMed=12477932;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullahy S.J.,
RA Basak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Mediates caspase-dependent apoptosis.
CC -!- SUBUNIT: Homodimer. Binds BAX, BCL2 and BCLX (By similarity).
CC -!- DOMAIN: The BH3-like domain is required for association with BAX
CC and for mediating apoptosis. The three BH domains (BH1, BH2, and
CC BH3) of BAX are all required for mediating protein-protein
CC interaction (By similarity).
CC -!- SIMILARITY: Belongs to the PMA family.
CC
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CC
CC EMBL; AF305551; AAC31787.1; -
CC DR EMBL; AK019599; BAB31810.1; -
CC DR EMBL; BC014715; AAH14715.1; -
CC DR EMBL; BC055374; AAH55374.1; -
CC DR MGD; MGI:1915555; Woapl.
CC KW Apoptosis.
FT SITE 120 127 BH3-LIKE.
FT DOMAIN 335 340 POLY-GLU.
FT CONFLICT 57 57 R -> K (IN REF. 3; AAH55374).
FT SEQUENCE 352 AA; 39404 MW; 8F4630D080495D98 CRC64;
Query Match 29.3%; Score 711; DB 1; Length 352;
Best Local Similarity 42.2%; Pred. No. 2.8e-44;
Matches 151; Conservative 70; Mismatches 119; Indels 18; Gaps 7;
QY 1 MPTLLQWCRCGEHLNTRCMLIGIPDCGDEBFEETLQACRHLYRGVIGRMFRREE 60
DB 1 MTLLELDCWCRCMDNPRKALLVAGIPTTCGVADIEALQAGLAPLGEHLLGRMFRDE 60
QY 61 NQAAILLELAQDIDYALLPRIPCKGGPWEIVKPRNSDGFELNRLNRFLEERRTVSDM 120
DB 61 NKNVALIGLTVETGSALVPKEIPAKGGVMRVIFKPPDTSDFLCRLNFEFLKGEQTMGEL 120
QY 121 NRVLGS-----DTNCSAPRTVISPEFWTQAQTLGAAPQLLEOMLYRELRFVSGNTIS 173
DB 121 TRVLGNRNDPLGLDPGIMPIR-APML--AAQALNEALKTLQVLYRYKLVSVSGRDP 176
QY 174 IPGALAFDAWLEHTTEMLOMQWQVEGEKRRKLMECLRGPAQGVSVGLNASIVTEBCL 233
DB 177 GPGEFEFESWFMFTSQVMKTVQWSDVEKRRRLIESLRGPAFEIIRVLKINPNFIVABCL 236
QY 234 AALQVQFQFVESHKTAQVKLCKAQEAGEKVSFVIRLEPLLQRAVENNVVSRNVNQTR 293

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DB 237 KTLTFIIGIINDPRALQVKLYLTYYQTKDEKLSAYVLLEPLQLXVKGKALEKEVVNQAR 296
QY 294 LKRVLSGATLPDKLRDKLKMQRKPPGFLALVKLL--REEEWEATLPGDRESLEG 349
DB 297 LDQVIAGA-VHKSVRRELGL-PEGSPAPGLQLTLTKKEAEEVEVLL---QAELEG 349

RESULT 10
ID LAM3 MOUSE STANDARD; PRT; 474 AA.
AC P48680;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lamin B3.
GN LMNB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93154351; PubMed=8094052;
RA Furukawa K., Hotta Y.;
RT "cDNA cloning of a germ cell specific lamin B3 from mouse
RT spermatocytes and analysis of its function by ectopic expression in
RT somatic cells.";
RL EMBO J. 12:97-106 (1993).
CC -!- FUNCTION: Lamins are components of the nuclear lamina, a fibrous
CC layer on the nucleoplasmic side of the inner nuclear membrane,
CC which is thought to provide a framework for the nuclear envelope
CC and may also interact with chromatin.
CC -!- SUBCELLULAR LOCATION: Nucleoplasmic side of the inner nuclear
CC membrane.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=B3;
CC IsoId=P48680-1; Sequence=Displayed;
CC Name=B2;
CC IsoId=P21619-1; Sequence=External;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Germ cell specific.
CC -!- PTM: B-TYPE LAMINS UNDERGO A SERIES OF MODIFICATIONS, SUCH AS
CC FARNESYLATION AND PHOSPHORYLATION. INCREASED PHOSPHORYLATION OF
CC THE LAMINS OCCURS BEFORE ENVELOPE DISINTEGRATION AND PROBABLY
CC PLAYS A ROLE IN REGULATING LAMIN ASSOCIATIONS.
CC -!- MISCELLANEOUS: The structural integrity of the lamina is strictly
CC controlled by the cell cycle, as seen by the disintegration and
CC formation of the nuclear envelope in prophase and telophase,
CC respectively.
CC -!- SIMILARITY: Belongs to the intermediate filament family. THIS IS A
CC B TYPE LAMIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D13455; BAA02708.1; -.
CC PIR; S28419; S28419.
CC MGD; MGI:96796; Lmnb2.
CC GO; GO:0005638; C:lamin filament; IDA.
CC InterPro; IPR001664; IF.
CC InterPro; IPR001322; IF_tail_C.
CC Pfam; PF00038; filament; 1.
CC Pfam; PF00932; IF_tail; 1.
CC PROSITE; PS00226; IF; 1.
CC Intermediate filament; Coiled coil; Nuclear protein; Lipoprotein;
CC Prenylation; Phosphorylation; Alternative splicing.

```

FT DOMAIN 1 26 HEAD.
 FT DOMAIN 27 256 ROD.
 FT DOMAIN 257 474 TAIL.
 FT DOMAIN 27 61 COIL 1A.
 FT DOMAIN 62 112 LINKER 12.
 FT DOMAIN 113 256 COIL 2.
 FT DOMAIN 275 281 POLY-SER.
 FT DOMAIN 293 298 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 443 456 ASP/GLU-RICH
 (HIGHLY ACIDIC, COULD BE INVOLVED IN
 CHROMATIN BINDING).
 FT LIPID 471 471 S-farnesyl cysteine (By similarity).
 SQ SEQUENCE 474 AA; 53268 MW; 9303CBEC3C77DE75 CRC64;

Query Match 4.7%; Score 114.5; DB 1; Length 474;
 Best Local Similarity 23.9%; Pred. No. 0.64;
 Matches 86; Conservative 48; Mismatches 147; Indels 79; Gaps 18;

QY 145 AQTGAAVQPLLEQMLYRELRF-----SGNT-----ISIPGALAFD-AMLEHTTEML 191
 Db 22 ARPLMETVEGALPELGRPLREYVRRPRGLGKTPVEDPVKSGAVGYPRTNNHLRVPT 81
 QY 192 QMWQVPEGEKR--RRLMECLRGPALQVSGLRASNAITVEECLAL-----QQV-FGPV 243
 Db 82 REQEVRETRRRHRRIVE-----VDSRQOEYDFRMAQALEDLRSQHDEQVRLYR 132
 QY 244 ESHKIAQVKL-----CKAQKAGEKVSFVLRLEPL-----LOR---AVENNVV 284
 Db 133 ELEQTYQAKLDNAKLLSDQNDKAAHARELKEARVRESLSYOLLGLOKQASAAENHI- 191
 QY 285 SRNVNQTLLKRVLSGATLPDKLKDLMKQRRKPPGFALIVKLRLREEEWEATLGPD- 343
 Db 192 -----HELEALAGER--DKFRKMLDAKEQEMTEVRDAMQQAELAEYQELLDIKLADM 242
 QY 344 -----RESLEG-----LEVAPRPARTIGVAPLPSGNSFPARPSQY--RRRRGQHR 393
 Db 243 ETSAYRKLLEGEERELKSPSSSRITISRATSSSSSGVGMVSGQGRKRLETEPT 302
 QY 394 RGGVARAG--SRGSRKRKHTFCYSCGEDGHRVQCINPNSLLLVKKQQAQAVESGNW 451
 Db 303 SGSPSRASVSSGSLAQTV-----ATGVNIDEVDPEG-RFVRLKNSDKDQSLGNW 355

RESULT 11
 ENGA RHIME STANDARD; PRT; 476 AA.
 ID ENGA RHIME
 AC Q92UK6
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 DE GTP-binding protein engA.
 GN ENGA OR RB1121 OR SMB20995.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OG Plasmid pSymb (megaplasmid 2).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=213396508; PubMed=11481431;
 RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
 RA Vorhoeiter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
 RA Golding B., Puehler A.;
 RT "The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-
 RT fixing endosymbiont Sinorhizobium meliloti";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
 CC -!- FUNCTION: Graft of unknown physiological role.
 CC -!- SIMILARITY: Belongs to the era/trmE family of GTP-binding
 CC proteins. EngA subfamily.
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 CC -----
 DR EMBL; AL603646; CAC49521.1; -;
 DR PIR; A95982; A95982.
 DR HAMAP; MF_00195; -; 1.
 DR InterPro; IPR005289; GTP-binding_dom.
 DR InterPro; IPR006073; GTP_OBG.
 DR InterPro; IPR002917; MMR_HSR1.
 DR InterPro; IPR001806; Ras_trnsmg.
 DR InterPro; IPR005225; Small_GTP.
 DR Pfam; PF01326; MMR_HSR1; 1.
 DR PRINTS; PR00326; GTP_OBG.
 DR PRINTS; PR00449; RASTRNSFRMG.
 DR TIGRFAMs; TIGR00650; MG442; 2.
 DR TIGRFAMs; TIGR00231; small_GTP; 2.
 KW GTP-binding; Repeat; 16; Plasmid; Complete proteome.
 FT NP_BIND 9 16 GTP 1 (POTENTIAL).
 FT NP_BIND 56 60 GTP 1 (POTENTIAL).
 FT NP_BIND 119 122 GTP 1 (POTENTIAL).
 FT NP_BIND 211 218 GTP 2 (POTENTIAL).
 FT NP_BIND 258 262 GTP 2 (POTENTIAL).
 FT NP_BIND 323 326 GTP 2 (POTENTIAL).
 SQ SEQUENCE 476 AA; 52965 MW; 0F6A150ED18F89B6 CRC64;

Query Match 4.7%; Score 113; DB 1; Length 476;
 Best Local Similarity 23.7%; Pred. No. 0.83;
 Matches 88; Conservative 41; Mismatches 101; Indels 142; Gaps 24;

QY 80 REIPGKG-----GPWEYIVKPRNSDGEFLNRLNLEERETVSDMNRVLGS 126
 Db 183 RPVAGEGTEDEVREPAYDETFLRVAIVGRPNAGK-STLINRFLGDR-----LLT 232
 QY 127 DTNCSAPRVITISPEFTWA-----QTLG-----AAVQPLLEQM-----LYRELRFSGNT 171
 Db 233 GPEAGITRDSIVE-WDMRGRTIKMFDTAGMRKAKVQEKLEKLSVADALRAIR-PAETV 230
 QY 172 I-----STP-----GALAFDAMLEHTTEMLQWQ-----VPEGEKRRRL 205
 Db 291 VIVFDATIPFEKQDLQIVDLVLRGAAVAFNFW-----DLVENQALLVDLREKTERL 345
 QY 206 MECLRGPALQVSGLRASNAITVECLAAQQVGPVESHKIAQVKLCQAQGEKVS 265
 Db 346 LPQAR-----GIRAV-----PISGH-----TGY----- 363
 QY 266 SFVLRLLEPLQRAVENNVSRNVNQTLLKRVLSGATL-----PDKL-----RDKLKLKMQ-RR 318
 Db 364 ---GLDRLMQAIETDKVWNERISTARLNRLWLESQQVQHPPPAVSGRLKLYMTQVKA 419
 QY 319 KPPGFLALVKLLREEEWEATLGPRESLEGLE-----VAPRPARTIGVAVPLPSGNSF 375
 Db 420 RPPGF--MISCTRPEAVPESEY---TRYLINGLRNDFLPGVPIR-----VHFRASENDF 468
 QY 376 DARPSQGYRRRR 387
 Db 469 ESKA-----RRKR 476

RESULT 12
 SPCR HUMAN
 ID SPCR HUMAN STANDARD; PRT; 3674 AA.
 AC Q9NEC6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Spectrin beta chain, brain 4 (Spectrin, non-erythroid beta chain 4)
 DE (Beta-v spectrin) (BSPECV).
 GN SPTEN5 OR SPTEN4
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cerebellum, Retina, and Spinal cord;
 RX MEDLINE=20347255; PubMed=10764729;
 RA Stabach P.R.; Morrow J.S.;
 RT "Identification and characterization of beta V spectrin, a mammalian
 ortholog of Drosophila beta H spectrin.";
 RL J. Biol. Chem. 275:21385-21395(2000).
 CC -!- SUBUNIT: Probably associates with an alpha chain.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Detected prominently in the
 outer segments of photoreceptor rods and cones and in the
 basolateral membrane and cytosol of gastric epithelial cells.
 CC -!- TISSUE SPECIFICITY: Expressed at very low levels in many tissues,
 with strongest expression in cerebellum, spinal cord, stomach,
 pituitary gland, liver, pancreas, salivary gland, kidney, bladder,
 and heart.
 CC -!- SIMILARITY: Belongs to the spectrin family.
 CC -!- SIMILARITY: Contains 2 calponin-homology (CH) domains.
 CC -!- SIMILARITY: Contains 1 PH domain.
 CC -!- SIMILARITY: Contains 31 spectrin repeats.
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 DR EMBL; AF233523; AAF65317.1; .
 DR HSPSP; Q01082; 1BKX.
 DR Genew; HGNC:15680; SPTEN5.
 DR MIM; 605916; .
 DR GO; GO:0016020; C:membrane; NAS.
 DR GO; GO:0008091; C:spectrin; NAS.
 DR GO; GO:0003779; F:actin binding; NAS.
 DR GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; NAS.
 DR InterPro; IPR001589; Actbind actinin.
 DR InterPro; IPR001715; Calponin-like.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR002017; Spectrin.
 DR InterPro; IPR001605; Spectrin_PH.
 DR Pfam; PF00307; CH; 2.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00435; spectrin; 30.
 DR PRINTS; PR00683; SPECTRINPH.
 DR SMART; SM00033; CH; 2.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00150; SPEC; 29.
 DR PROSITE; PS00019; ACTININ_1; 1.
 DR PROSITE; PS00020; ACTININ_2; FALSE_NEG.
 DR PROSITE; PS00021; CH; 2.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 KW Cytoskeleton; Membrane; Repeat; Actin-binding; Actin capping.
 FT DOMAIN 1 279 ACTIN-BINDING (BY SIMILARITY).
 FT DOMAIN 54 159 CH 1.
 FT DOMAIN 177 279 CH 2.
 FT REPEAT 106 416 SPECTRIN 1.
 FT REPEAT 426 531 SPECTRIN 2.
 FT REPEAT 533 637 SPECTRIN 3.
 FT REPEAT 639 743 SPECTRIN 4.
 FT REPEAT 745 810 SPECTRIN 5.
 FT REPEAT 867 894 SPECTRIN 6.
 FT REPEAT 896 998 SPECTRIN 7.
 FT REPEAT 1102 1206 SPECTRIN 8.
 FT REPEAT 1208 1312 SPECTRIN 9.
 FT REPEAT 1314 1417 SPECTRIN 10.
 FT REPEAT 1419 1488 SPECTRIN 11.
 FT REPEAT 1520 1624 SPECTRIN 12.
 FT REPEAT 1626 1728 SPECTRIN 13.
 FT REPEAT 1730 1835 SPECTRIN 14.
 FT REPEAT 1837 1941 SPECTRIN 15.
 FT REPEAT 1943 2047 SPECTRIN 16.
 FT REPEAT 2049 2147 SPECTRIN 17.
 FT REPEAT 2149 2253 SPECTRIN 18.
 FT REPEAT 2255 2301 SPECTRIN 19.
 FT REPEAT 2314 2362 SPECTRIN 20.
 FT REPEAT 2364 2468 SPECTRIN 21.
 FT REPEAT 2470 2574 SPECTRIN 22.
 FT REPEAT 2576 2680 SPECTRIN 23.
 FT REPEAT 2682 2785 SPECTRIN 24.
 FT REPEAT 2787 2891 SPECTRIN 25.
 FT REPEAT 2893 2997 SPECTRIN 26.
 FT REPEAT 2999 3103 SPECTRIN 27.
 FT REPEAT 3105 3210 SPECTRIN 28.
 FT REPEAT 3212 3312 SPECTRIN 29.
 FT REPEAT 3314 3418 SPECTRIN 30.
 FT REPEAT 3420 3482 SPECTRIN 31.
 FT DOMAIN 3533 3641 PH.
 SQ SEQUENCE 3674 AA; 416832 MW; 8C0FDFAD0DD0C7C18 CRC64;
 Query Match 4.7%; Score 113; DB 1; Length 3674;
 Best Local Similarity 21.0%; Pred. No. 12;
 Matches 93; Conservative 63; Mismatches 155; Indels 132; Gaps 22;
 QY 36 EETLQEAQRHLGRYRVIGRMFRRENAQAAILL-----ELAQDIDYALLPR----- 80
 Db 1332 EKLMAAHEPSGARRNLQTLKRHEAASELLATRRHVEALQVGRELLSRPCGQEDIQ 1391
 QY 81 -EIPGKGPMVEIVKPRNSDGEFL-----NRLNRFLFEERTVSDMNRVL-----GSDT 128
 Db 1392 TRLQGLRSKWEALNRKWTGDELQQAQGBQLLRQLQDAKEQLQLEGALQSSETGDL 1451
 QY 129 NCSAPRTVISPEFTWTAQL-----GAAVQPLLE--OMLYRELRFVSGNTIS 173
 Db 1452 RSSQRLQKRHQQLSESRITLAAKMAALASMAHGMAASPAILEETQKHLRLELQGH-LA 1510
 QY 174 IPGALAFDAWLE-----HTTEMLQW--OVPEGEKRRRLMECLRG-----PALQV- 216
 Db 1511 IRG-LQQAQVELHQFCHLSNMELSWAEHPHSP-TSYTECLNGAQLSRKHKHKLQVE 1568
 QY 217 -----VSLGRASNASIT-----VBECLAAQQVFPVESHKIAQVKLCAYQE 259
 Db 1569 VKAHQGVQVRLSSGRSLAASGHFQAQHVQEC-----QELGHWAEELERACEARAQ 1620
 QY 260 AGEKVSSF-----VLRLE-----PLL-----ORAVENNVSRNVNTRL----- 294
 Db 1621 CLOQAVTFQYFLDVSELEGWVEEKLPLVSSRDYGRDEATRLINKHQAQLELAIVWS 1680
 QY 295 -----KRVLSGATLP-----DKLRDKLKMKQ-----RRKPPGFLALVKLLREEE 334
 Db 1681 SMEELDTQAQLTGPEVPEQQRVVQERLREQRLALQELAAATDRLEGLTLRHEFLREAE 1740
 QY 335 EWEATLGPDRSLEGLVAPRPP 357
 Db 1741 DLQGLASQKQAAKGESLGEDP 1763
 RESULT 13
 CK13 HUMAN
 ID CK13 HUMAN STANDARD; PRT; 373 AA.
 AC Q02833;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein C11orf13 (HRAS1-related cluster protein 1).
 GN C11orf13 OR HRC1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Placenta;


```

Db 309 ---EAEK---LVASLDSSLEEBQFTAAQTQGLRHSAANTALPLSHGAARKWFYKDPQG 362
QY 241 ---GPVESHKIAQ---VKL-C-KAYQEAQGVSVFLRL----- 271
Db 363 EIQQPFTTQMAEWFAQYFMSLLVKGCDGEGQPLGE---VIKMGCRVPPAPGPSP 417
QY 272 EPLLORAVENNVSRNNQTRLKR--VLSGATLPDKLRK--LKLKMKQRKPPGFLALV 327
Db 418 PPLL-----GNMDOERLKKQOELAAALYQQLQHQFQLQVSSRQLPQ----- 460
QY 328 KLIREEEWEATLGPDRLESLGLEVAVRPP-----ARITGVGAVPLPASGNSFD 376
Db 461 CALRE-----KAALG-----DLTPPPPPPPQQOQLTAFLOQLKXPPSS----- 502
QY 377 ARPSQGYRRRGRGQHRGGVARAGSRGSRKRKHTFCYSGEDGHIRVQCINPS 431
Db 503 -RSAEKSSGRS-GRKNASVRSASSSRRSR-----SGRRRKSCFGAS 547

RESULT 15
SSB DEIRA
ID SSB DEIRA STANDARD; PRT; 301 AA.
AC Q9RY51:
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Single-strand binding protein (SSB) (Helix-destabilizing protein).
GN SSB OR DR0099.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RA Witte G., Urbanke C., Curth U.;
RT "Single-stranded DNA binding protein from Deinococcus radiodurans - Cloning, expression and biophysical characterization.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RA Egginton J.M., Wood E.A., Cox M.M.;
RT "The Deinococcus radiodurans ssb gene encodes a contiguous ORF for single-stranded DNA-binding protein.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vanatavean J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
RL Science 286:1571-1577(1999).
CC !- FUNCTION: This protein is essential for replication of the chromosome. It is also involved in DNA recombination and repair (By similarity).
CC !- SUBUNIT: Homodimer (By similarity).
CC !- SIMILARITY: Contains 2 SSB domains.
CC !- CAUTION: Ref.3 sequence differs from that shown due to two frameshifts in positions 93 and 169.
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CC -----
DR EMBL; AJ564860; CAD92322.1; -.
DR EMBL; AY293617; AAQ18705.1; -.
DR EMBL; AE001873; AAF09692.1; ALT_FRAME.
DR EIR; A75559; A75559.
DR HSP; P02339; IKAW.
DR TIGR; DR0099; -.
DR InterPro; IPR008994; Nucleic acid OB.
DR InterPro; IPR000424; SSB_protein.
DR Pfam; PF00436; SSB; 1.
DR PROSITE; PS00935; SSB; 2.
KW DNA-binding; DNA repair; DNA replication; Complete proteome; Repeat.
FT DOMAIN 5 110
FT DOMAIN 129 232
FT SEQUENCE 301 AA; 32722 MW; 21B2090C970E1B0E CRC64;
SQ
Query Match 4.4%; Score 106.5; DB 1; Length 301;
Best Local Similarity 25.5%; Pred. No. 1.3; Indels 93; Gaps 21;
Matches 80; Conservative 39; Mismatches 102;
QY 116 TVSDMRVLGSD-TNCSAP---RVTI--SPEFTWQTLGAAVQPLLEQMLYRELRFVSG 169
Db 33 TVAGEDRVIGNDGRERNLPWVHRVSLGKPAEW-----QAERNLKGK 74
QY 170 NTSIPGALAFDAWLEHTTEMLQWQVPEGEKRRRL-MECLR-----GPAQVQV---SGL 220
Db 75 DAVVVEGTLEY-----RQWEAPEGGKRSVNVKALRMBQLGTPELIQDAGGV 123
QY 221 RASNASITVEECLAALQOVFGPVBESHKIAQVKLCKAYQEAQGVSVFLRLEPLLRQAVE 280
Db 124 RMSGA---MEVL-----VLGNVT--RDPEIR---YTPAGDAVLS-----LSIAVN 161
QY 281 NNVSRRNVNQLRLKRVLSGATLPDKLRDKLKLKMKQRKPPGFLALVKLREBEWEATL 340
Db 162 ENYQDRQGQKQKVHYI--DATL---WRDLAENMKELRKGPVVMIMGLV--NEGWTDKD 214
QY 341 GPDRESLEGLEVAVRPPPARITGVG-----AVPLPASGN-----SFDARP-SQGYRRRRGR 389
Db 215 GNKENSTR--VEATRVLEALFARGAGNANSYAAATPAAPRTQTATSSAARPTSGGYQSQPSR 272
QY 390 GQHRGGVARAGSR 403
Db 273 -----AANTGSR 279
Search completed: September 27, 2004, 17:08:48
Job time : 18.1307 secs

```

Blank

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 17:05:06 ; Search time 58.2533 Seconds
(without alignments)
2507.755 Million cell updates/sec

Title: US-10-037-860-13

Perfect score: 2423
Sequence: 1 MPTLLQDWCGRGHEHLNTRRC.....VESGNGNWAWDKSHPKSKAK 463

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2423	100.0	463	Q9UL41	Q9ul41 homo sapien
2	2283.5	94.2	455	Q9H0A4	Q9h0a4 homo sapien
3	1796.5	74.1	466	Q8JZW8	Q8jzw8 mus musculu
4	883.5	36.5	448	Q8NET3	Q8net3 homo sapien
5	883.5	36.5	452	Q96PV4	Q96pv4 homo sapien
6	836.5	34.5	364	Q94959	Q94959 homo sapien
7	826.5	34.1	364	Q9GMU3	Q9gm3 macaca fasc
8	824	34.0	353	Q9CYP2	Q9cyp2 mus musculu
9	822	33.9	353	Q8VH24	Q8vh24 rattus norv
10	822	33.9	353	Q8CLC8	Q8clc8 mus musculu
11	818	33.8	353	Q8NG07	Q8ng07 homo sapien
12	816	33.7	353	Q95144	Q95144 homo sapien
13	793	32.7	150	Q9BE35	Q9be35 macaca fasc
14	768.5	31.7	351	Q96BY2	Q96by2 homo sapien
15	768.5	31.7	399	Q96A40	Q96a40 homo sapien
16	763.5	31.5	351	Q9HAS1	Q9has1 homo sapien

17	761.5	31.4	351	6	Q9SKI4	Q9sk14 macaca fasc
18	725.5	29.9	365	11	Q8BHK0	Q8bhk0 mus musculu
19	711	29.3	352	11	Q9ERH6	Q9erb6 mus musculu
20	618.5	25.5	283	4	Q9UL42	Q9ul42 homo sapien
21	470.5	19.4	402	11	Q9CZA5	Q9cza5 mus musculu
22	454.5	18.8	237	4	Q9H833	Q9h833 homo sapien
23	449.5	18.6	194	4	Q95145	Q95145 homo sapien
24	425.5	17.6	192	4	Q8ND90	Q8nd90 homo sapien
25	423.5	17.5	403	4	Q8TE36	Q8te36 homo sapien
26	415.5	17.1	402	4	Q8NIC1	Q8nic1 homo sapien
27	390.5	16.1	393	11	Q9DB17	Q9db17 mus musculu
28	390.5	16.1	393	11	Q8VD24	Q8vd24 mus musculu
29	351.5	14.5	378	4	Q8N3H4	Q8nv39 homo sapien
30	351.5	14.5	435	4	Q8V59	Q8v59 homo sapien
31	339.5	14.0	430	11	Q8VNM8	Q8vnm8 mus musculu
32	333.5	13.8	246	11	Q8C533	Q8c533 mus musculu
33	323	13.3	149	4	Q9UL43	Q9ul43 homo sapien
34	202	8.3	327	11	Q8VC32	Q8vc32 mus musculu
35	191	7.9	538	4	Q9H0W5	Q9h0w5 homo sapien
36	191	7.9	538	4	Q8TB26	Q8tb26 homo sapien
37	156	6.4	1394	10	Q8H8L9	Q8h8l9 oryza sativ
38	156	6.4	1433	10	Q942G3	Q942g3 oryza sativ
39	149	6.1	1715	10	Q8H870	Q8h870 oryza sativ
40	148	6.1	1661	10	Q7XBQ6	Q7xbq6 oryza sativ
41	145	6.0	1594	10	Q8LN00	Q8ln00 oryza sativ
42	144.5	6.0	1449	10	Q8SK3	Q8sk3 oryza sativ
43	142.5	5.9	1742	10	Q7XLU2	Q7xlu2 oryza sativ
44	142	5.9	1466	10	Q7XGE5	Q7xge5 oryza sativ
45	142	5.9	1616	10	Q7XW87	Q7xw87 oryza sativ

ALIGNMENTS

RESULT 1

Q9UL41 PRELIMINARY; PRT; 463 AA.

AC Q9UL41, 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Paraneoplastic neuronal antigen MA3.

GN MA3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Gultekin S.H., Voltz R., Rosenfeld M.R., Gerstner E., Eichen J.,

RA Posner J.B., Dalmay J.;

RT "Identification of a novel cancer testis brain antigen using serum

RT antibodies from patients with testicular tumors and paraneoplastic

RT limbic encephalomyelitis";

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF083116; AAF05627.1; -;

DR Genbank; HGNC:18742; FNMA3.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR InterPro; IPR001878; Znf_CCHC.

DR Pfam; PF00098; zf-CCHC; 1.

DR PRINTS; PR00939; C2HCZNFINGER.

DR SMART; SM00343; Znf_C2HC; 1.

DR PROSITE; PS50158; ZF_CCHC; 1.

SQ SEQUENCE 463 AA; 52376 MW; 0843EF6601D8557C CRC64;

Query Match 100.0%; Score 2423; DB 4; Length 463;

Best Local Similarity 100.0%; Pred. No. 3.2e-185;

Matches 463; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPTLLQDWCGRGHEHLNTRRCMLILGIPDCGEDEFEETLQACRHLGRYVIGRMFRREE 60

Db 1 MPTLLQDWCGRGHEHLNTRRCMLILGIPDCGEDEFEETLQACRHLGRYVIGRMFRREE 60

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QY 61 NAQAIILELAQDIDYALLPREIFKGGPWEVIVKPRNSDGEFLNRLNRFLEEBERTVSDM 120
Db 61 NAQAIILELAQDIDYALLPREIFKGGPWEVIVKPRNSDGEFLNRLNRFLEEBERTVSDM 120
QY 121 NRVLGSDTNCAPRVITISPEFWTWAQTLGAAVQPLLEQMLYRELRFVSGNTTISIPGALAF 180
Db 121 NRVLGSDTNCAPRVITISPEFWTWAQTLGAAVQPLLEQMLYRELRFVSGNTTISIPGALAF 180
QY 181 DAWLEHTTEMLQWQVPEGEKRRRLMECLRGPALQVVGSLRASNASTIVTECLAAALQOVF 240
Db 181 DAWLEHTTEMLQWQVPEGEKRRRLMECLRGPALQVVGSLRASNASTIVTECLAAALQOVF 240
QY 241 GPVESHKIAQVKLCKAYQAGEKVSFVLRLPQLQRAVENNVSRNNVQTRLKRVLSG 300
Db 241 GPVESHKIAQVKLCKAYQAGEKVSFVLRLPQLQRAVENNVSRNNVQTRLKRVLSG 300
QY 301 ATLPDKLRDKLKMQRKPPGFLALVKLLREEEWEATLGPDRSLEGLVAPRPPARI 360
Db 301 ATLPDKLRDKLKMQRKPPGFLALVKLLREEEWEATLGPDRSLEGLVAPRPPARI 360
QY 361 TGVGAVPLPASGNSFDARPSQGYRRRRGRGQHRGGVARAGSGSRKRKHTTCYSCGD 420
Db 361 TGVGAVPLPASGNSFDARPSQGYRRRRGRGQHRGGVARAGSGSRKRKHTTCYSCGD 420
QY 421 GHIRVQCINPSNLLLVKQKQAAVESGNGWMDKSHPKSKAK 463
Db 421 GHIRVQCINPSNLLLVKQKQAAVESGNGWMDKSHPKSKAK 463

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RESULT 2

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Q9HOA4 PRELIMINARY; PRT; 455 AA.
ID Q9HOA4
AC Q9HOA4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN DKFZP344K25.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21154917; PubMed=11230166;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansoerge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,
RA Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a Catalog of Human Genes and Proteins: Sequencing and
RT Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
RL Genome Res. 11:422-435 (2001).
DR EMBL; ALI36878; CAB6812.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001878; Znf CCHC.
DR Pfam; PF00098; zf-CCHC; 1.
DR SMART; SM00343; Znf C2HC; 1.
DR PROSITE; PS0158; ZF_CCHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 455 AA; 51514 MW; 9AC8CC06685A8956 CRC64;

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Query Match 94.2%; Score 2283.5; DB 4; Length 455;
Best Local Similarity 98.2%; Pred. No. 4.5e-174;
Matches 439; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 MPTLLQDWCRCGEHLNTRCMLILGIPDCGDEFEETLQEAACHLGRYVIGRMFRREE 60
Db 1 MPTLLQDWCRCGEHLNTRCMLILGIPDCGDEFEETLQEAACHLGRYVIGRMFRREE 60
QY 61 NAQAIILELAQDIDYALLPREIFKGGPWEVIVKPRNSDGEFLNRLNRFLEEBERTVSDM 120

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Db 61 NAQAIILELAQDIDYALLPREIFKGGPWEVIVKPRNSDGEFLNRLNRFLEEBERTVSDM 120
QY 121 NRVLGSDTNCAPRVITISPEFWTWAQTLGAAVQPLLEQMLYRELRFVSGNTTISIPGALAF 180
Db 121 NRVLGSDTNCAPRVITISPEFWTWAQTLGAAVQPLLEQMLYRELRFVSGNTTISIPGALAF 180
QY 181 DAWLEHTTEMLQWQVPEGEKRRRLMECLRGPALQVVGSLRASNASTIVTECLAAALQOVF 240
Db 181 DAWLEHTTEMLQWQVPEGEKRRRLMECLRGPALQVVGSLRASNASTIVTECLAAALQOVF 240
QY 241 GPVESHKIAQVKLCKAYQAGEKVSFVLRLPQLQRAVENNVSRNNVQTRLKRVLSG 300
Db 241 GPVESHKIAQVKLCKAYQAGEKVSFVLRLPQLQRAVENNVSRNNVQTRLKRVLSG 300
QY 301 ATLPDKLRDKLKMQRKPPGFLALVKLLREEEWEATLGPDRSLEGLVAPRPPARI 360
Db 301 ATLPDKLRDKLKMQRKPPGFLALVKLLREEEWEATLGPDRSLEGLVAPRPPARI 360
QY 361 TGVGAVPLPASGNSFDARPSQGYRRRRGRGQHRGGVARAGSGSRKRKHTTCYSCGD 420
Db 361 TGVGAVPLPASGNSFDARPSQGYRRRRGRGQHRGGVARAGSGSRKRKHTTCYSCGD 420
QY 421 GHIRVQCINPSNLLLVKQKQAAVESG 447
Db 421 GHIRVQCINPSNLLLVKQKQAAVESG 446

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RESULT 3

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Q8JZW8 PRELIMINARY; PRT; 466 AA.
ID Q8JZW8
AC Q8JZW8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to paraneoplastic antigen MA3.
GN PMA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Strausberg R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC036726; AAH36726.1; -.
DR MGD; MGI:2180565; Pma3.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001544; Aminotrans IV.
DR InterPro; IPR001878; Znf CCHC.
DR Pfam; PF00098; zf-CCHC; 1.
DR PRINTS; PR00939; C2HCZNFINGER.
DR PROSITE; PS0158; ZF_CCHC; 1.
SQ SEQUENCE 466 AA; 54040 MW; 113787E37B0B3AAD CRC64;

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Query Match 74.1%; Score 1796.5; DB 11; Length 466;
Best Local Similarity 73.4%; Pred. No. 4e-135;
Matches 345; Conservative 49; Mismatches 65; Indels 11; Gaps 4;

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QY 1 MPTLLQDWCRCGEHLNTRCMLILGIPDCGDEFEETLQEAACHLGRYVIGRMFRREE 60
Db 1 MPTLLQDWCRCGEHLNTRCMLILGIPDCGDEFEETLQEAACHLGRYVIGRMFRREE 60
QY 61 NAQAIILELAQDIDYALLPREIFKGGPWEVIVKPRNSDGEFLNRLNRFLEEBERTVSDM 120
Db 61 NAQAIILELAQDIDYALLPREIFKGGPWEVIVKPRNSDGEFLNRLNRFLEEBERTVSDM 120
QY 121 NRVLGSDTNCAPRVITISPEFWTWAQTLGAAVQPLLEQMLYRELRFVSGNTTISIPGALAF 180
Db 121 NRVLGSDTNCAPRVITISPEFWTWAQTLGAAVQPLLEQMLYRELRFVSGNTTISIPGALAF 180

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181 DAWLEHTTEMLQMWQVPEGEKRRRLMECLRGPALQVVGSLRAGNASITVBECLAAQQVF 240
181 DSWLEHTTEMLQMWQVPEGEKRRRLMECLRGPALQVVGSLRAGNASITVBECLAAQQVF 240
241 GPVESHKIAQVKLCAYQAGEKVSFVLRLPQLQAVENNVSRNNVOTRLKRVLSG 300
241 GSDVNRKIAQVKFCAYQAGEKVSFVLRLPQLQAVENNVSRNNVOTRLKRVLSG 300
301 ATLDPKLRDLKLMKQRRKPPGFLALVKLLR-BEEWEATLGPDRSLEGLVAPRPPAR 359
301 AILSAKUREKLMKQRRKPPGFLALVKLLR-BEEWEATLGPDRSLEGLVAPRPPAR 359
360 ITGVGA-----VPLPASGNSFDARPSQGYRR--RGRGHRGGVVARAGSRGRKRRHTF 413
368 -SNIGSEERELFVPAFGSVLEERPYQCSRRRRHRRGQHRKGGVPRDSSQGRKQNYDTF 416
414 CYSCEGDGHIRVQCINPSNLLLVKQKQAAVESGNGWAKDHPKSKAK 463
417 CYSCEGDGHIRVHCNPSNRLVTKQKQAAVEKNGRSMWAKDHPKSKAK 466

RESULT 4
Q8NET3 PRELIMINARY; PRT; 448 AA.
AC Q8NET3
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE BJ-HCC-25 tumor antigen.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xueyuan D., Weifeng C.;
RT "Cloning and identification of genes which are differentially
RT expressed in carcinoma."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY121806; AAM82754.1; --
SQ SEQUENCE 448 AA; 49334 MW; 5F6BC8A15B457A89 CRC64;

Query Match 36.5%; Score 883.5; DB 4; Length 448;
Best Local Similarity 42.6%; Pred. No. 3.7e-62;
Matches 201; Conservative 75; Mismatches 155; Indels 41; Gaps 10;

Qy 1 MPTLLQDWCRCGEHLNTRCMLILGIPEDCGEDEFETLQACRHLGRLYRVLGRMFRREE 60
Db 1 MALTLLDWCCKGMDMPKALLIVGIPMECSEVEIQDTVKAGLQPLCAYRVLGRMFRRED 60
61 NAOAILLEAQDIDYALLPREIPGKGGPWVIVKPRNSDGEFLNRLNRLFLBEERTVSDM 120
61 NAKAVFIELADTVNTTLPSHIPGKGGSWVIVKPRNPDDDFLRLNRYFLKDEGRSMTDV 120
121 NRVLGSDTNCAPRVITISPEFTWAQTGLAAVQPLLEQMLYRLRVFSGNTISIPGALAF 180
121 ARALGC--CSLPAESLDAE--VMPQVRSPPLEPPKESMWYRKLKVFSGTASPSPEET 175
181 DAWLEHTTEMLQMWQVPEGEKRRRLMECLRGPALQVVGSLRAGNASITVBECLAAQQVF 240
176 EDWLEQVTEIMPIWQVSEVEKRRRLLESIRGPAISIMRVLQANNDISITVEQCLDALKQIF 235
61 NAKAVFIELADTVNTTLPSHIPGKGGSWVIVKPRNPDDDFLRLNRYFLKDEGRSMTDV 120
121 NRVLGSDTNCAPRVITISPEFTWAQTGLAAVQPLLEQMLYRLRVFSGNTISIPGALAF 180
121 ARALGC--CSLPAESLDAE--VMPQVRSPPLEPPKESMWYRKLKVFSGTASPSPEET 175
181 DAWLEHTTEMLQMWQVPEGEKRRRLMECLRGPALQVVGSLRAGNASITVBECLAAQQVF 240
176 EDWLEQVTEIMPIWQVSEVEKRRRLLESIRGPAISIMRVLQANNDISITVEQCLDALKQIF 235
241 GPVESHKIAQVKLCAYQAGEKVSFVLRLPQLQAVENNVSRNNVOTRLKRVLSG 300
236 GKDVEDFRASQFRFLQTSPIKGEKVSTFLRLLEPLLQKAVHKSPLSVRSDMIRLKHLLAR 295
301 ATLDPKLRDLKLMKQRRKPPGFLALVKLLR-BEEWEATLGPDRSLEGLVAPRPPAR 356
296 VAMTPALRGKLELLDQRCPPNFLEMLKLRDEEWEATEAVMKNEKPSGRGRGASGRQ 355
357 PARITGVGAVPLPASGNSF-DARPS--QG-----YRRRGRGQHRGGVVARAGSRGRKR 408
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356 ARAEASVAPQATVQARSFSDSSPQTIOGGLPPLVKERR-----LLGSESTR-- 402
409 KRHTFCYSCGDGHIRVQCINPSNLLLVKQKQAAVES-GNGNWAWDKSHPK 459
403 -----GED-HGQATYPKAEQNTPGREGPQAAGEELGNEAGAGAMSHPK 444

RESULT 5
Q96PV4 PRELIMINARY; PRT; 452 AA.
AC Q96PV4
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein KIAA1934 (Fragment).
DE KIAA1934.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Nadase T., Kikuno R., Ohara O.;
RT MEDLINE=21456161; PubMed=11572484;
RT "Prediction of the coding sequences of unidentified human genes. XXI.
RT The complete sequences of 60 new cDNA clones from brain which code for
RT large proteins."
RL DNA Res. 8:179-187(2001).
DR EMBL: AB067521; BAB67827.1; --
DR Genbank: U08743; PNMAS.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 452 AA; 50289 MW; A7553ECE7CA751EA CRC64;

Query Match 36.5%; Score 883.5; DB 4; Length 452;
Best Local Similarity 42.6%; Pred. No. 3.7e-62;
Matches 201; Conservative 75; Mismatches 155; Indels 41; Gaps 10;

Qy 1 MPTLLQDWCRCGEHLNTRCMLILGIPEDCGEDEFETLQACRHLGRLYRVLGRMFRREE 60
Db 5 MALTLLDWCCKGMDMPKALLIVGIPMECSEVEIQDTVKAGLQPLCAYRVLGRMFRRED 64
61 NAOAILLEAQDIDYALLPREIPGKGGPWVIVKPRNSDGEFLNRLNRLFLBEERTVSDM 120
65 NAKAVFIELADTVNTTLPSHIPGKGGSWVIVKPRNPDDDFLRLNRYFLKDEGRSMTDV 124
121 NRVLGSDTNCAPRVITISPEFTWAQTGLAAVQPLLEQMLYRLRVFSGNTISIPGALAF 180
125 ARALGC--CSLPAESLDAE--VMPQVRSPPLEPPKESMWYRKLKVFSGTASPSPEET 179
181 DAWLEHTTEMLQMWQVPEGEKRRRLMECLRGPALQVVGSLRAGNASITVBECLAAQQVF 240
180 EDWLEQVTEIMPIWQVSEVEKRRRLLESIRGPAISIMRVLQANNDISITVEQCLDALKQIF 239
241 GPVESHKIAQVKLCAYQAGEKVSFVLRLPQLQAVENNVSRNNVOTRLKRVLSG 300
240 GKDVEDFRASQFRFLQTSPIKGEKVSTFLRLLEPLLQKAVHKSPLSVRSDMIRLKHLLAR 299
301 ATLDPKLRDLKLMKQRRKPPGFLALVKLLR-BEEWEATLGPDRSLEGLVAPRPPAR 356
300 VAMTPALRGKLELLDQRCPPNFLEMLKLRDEEWEATEAVMKNEKPSGRGRGASGRQ 359
357 PARITGVGAVPLPASGNSF-DARPS--QG-----YRRRGRGQHRGGVVARAGSRGRKR 408
360 ARAEASVAPQATVQARSFSDSSPQTIOGGLPPLVKERR-----LLGSESTR-- 406
409 KRHTFCYSCGDGHIRVQCINPSNLLLVKQKQAAVES-GNGNWAWDKSHPK 459
407 -----GED-HGQATYPKAEQNTPGREGPQAAGEELGNEAGAGAMSHPK 448

RESULT 6
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Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenwald C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz K., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK017476; BAB30762.1; --.
DR MGD; MGI:2180564; Pnmal.
SQ SEQUENCE 353 AA; 39718 MW; F7B27378B8469675 CRC64;

Query Match 34.0%; Score 824; DB 11; Length 353;
Best Local Similarity 49.4%; Pred. No. 1.5e-57;
Matches 175; Conservative 55; Mismatches 116; Indels 8; Gaps 4;

Qy 1 MPTLLQDWCRCGEHLNTRCMLILGIPDCGDEFEETLQACRHLGRLVGRVGRMFRREE 60
Db 1 MAMTLLDWCRCGMDVNSQRALLVWGIPVNCDETEIETLQAMPQVS--YRVLGRMFWREE 59

Qy 61 NAKAILELAQDIDYALLPREIPGKGGPWEIVKPRNSDGEFLNRLNRLNLEERRTVSDM 120
Db 60 NAKAALDELGTVDYSLIPREMPGKGLWKVFKPTSDAFLRLHLFLAREGWTQDV 119

Qy 121 NRVLGSDTNC SAPRVTISPEFWTWAQTLGAAVQPLLEQMLYRELRFVSGNTISIPGALAF 180
Db 120 ARVLGFQNPAPAPGPEPAEMLVN--ILDNVIQPLVESIWYKLTLPFGKDIIPGGEETF 177

Qy 181 DAWLEHTTEMLQMWQVPEGEKRRRLMECLRGPAQVSLGRASNASITVECLAAQOVF 240
Db 178 DSWLEHSENEIEEQQVSDIEKRRRLMESLRGPAADVIRILKTNPAITTAECLEKALEQV 237

Qy 241 GPVESHKIAQVKLCAYQAEAGEKVSFVLRLPELQRAVENNVSRNNVOTRLKRVLSG 300
Db 238 GSVESSRDAQVRFNTYQNPGEKLSYVIRLEPLQKVVKGIDKONVQARLEQVIAG 297

Qy 301 ATLDPKLRDLKLMKQRRKP--PGFLALVKKLRE---EWEATLGPDRSLEG 349
Db 298 ANHSGALRRQLWLTGATEGPAPNLFOLLVQIRREBEAKEEBAEAAALLQLGLEG 351

Query Match 33.9%; Score 822; DB 11; Length 353;
Best Local Similarity 49.4%; Pred. No. 2.2e-57;
Matches 175; Conservative 54; Mismatches 117; Indels 8; Gaps 4;

Qy 1 MPTLLQDWCRCGEHLNTRCMLILGIPDCGDEFEETLQACRHLGRLVGRVGRMFRREE 60
Db 1 MAMTLLDWCRCGMDVNSQRALLVWGIPVNCDETEIETLQAMPQVS--YRVLGRMFWREE 59

Qy 61 NAKAILELAQDIDYALLPREIPGKGGPWEIVKPRNSDGEFLNRLNRLNLEERRTVSDM 120
Db 60 NAKAALDELGTVDYSLIPREMPGKGLWKVFKPTSDAFLRLHLFLAREGWTQDV 119

Qy 121 NRVLGSDTNC SAPRVTISPEFWTWAQTLGAAVQPLLEQMLYRELRFVSGNTISIPGALAF 180
Db 120 ARVLGFQNPAPAPGPEPAEMLVN--ILDNVIQPLVESIWYKLTLPFGKDIIPGGEETF 177

Qy 181 DAWLEHTTEMLQMWQVPEGEKRRRLMECLRGPAQVSLGRASNASITVECLAAQOVF 240
Db 178 DSWLEHSENEIEEQQVSDIEKRRRLMESLRGPAADVIRILKTNPAITTAECLEKALEQV 237

Qy 241 GPVESHKIAQVKLCAYQAEAGEKVSFVLRLPELQRAVENNVSRNNVOTRLKRVLSG 300
Db 238 GSVESSRDAQVRFNTYQNPGEKLSYVIRLEPLQKVVKGIDKONVQARLEQVIAG 297

Qy 301 ATLDPKLRDLKLMKQRRKP--PGFLALVKKLRE---EWEATLGPDRSLEG 349
Db 298 ANHSGALRRQLWLTGATEGPAPNLFOLLVQIRREBEAKEEBAEAAALLQLGLEG 351

Query Match 33.9%; Score 822; DB 11; Length 353;
Best Local Similarity 49.2%; Pred. No. 2.2e-57;
Matches 174; Conservative 55; Mismatches 117; Indels 8; Gaps 4;

Qy 1 MPTLLQDWCRCGEHLNTRCMLILGIPDCGDEFEETLQACRHLGRLVGRVGRMFRREE 60
Db 1 MAMTLLDWCRCGMDVNSQRALLVWGIPVNCDETEIETLQAMPQVS--YRVLGRMFWREE 59

Qy 61 NAKAILELAQDIDYALLPREIPGKGGPWEIVKPRNSDGEFLNRLNRLNLEERRTVSDM 120
Db 60 NAKAALDELGTVDYSLIPREMPGKGLWKVFKPTSDAFLRLHLFLAREGWTQDV 119

Qy 121 NRVLGSDTNC SAPRVTISPEFWTWAQTLGAAVQPLLEQMLYRELRFVSGNTISIPGALAF 180
Db 120 ARVLGFQNPAPAPGPEPAEMLVN--ILDNVIQPLVESIWYKLTLPFGKDIIPGGEETF 177

Qy 181 DAWLEHTTEMLQMWQVPEGEKRRRLMECLRGPAQVSLGRASNASITVECLAAQOVF 240
Db 178 DSWLEHSENEIEEQQVSDIEKRRRLMESLRGPAADVIRILKTNPAITTAECLEKALEQV 237

Qy 241 GPVESHKIAQVKLCAYQAEAGEKVSFVLRLPELQRAVENNVSRNNVOTRLKRVLSG 300
Db 238 GSVESSRDAQVRFNTYQNPGEKLSYVIRLEPLQKVVKGIDKONVQARLEQVIAG 297

Qy 301 ATLDPKLRDLKLMKQRRKP--PGFLALVKKLRE---EWEATLGPDRSLEG 349
Db 298 ANHSGALRRQLWLTGATEGPAPNLFOLLVQIRREBEAKEEBAEAAALLQLGLEG 351

RESULT 10
Q8C1C8
ID Q8C1C8 PRELIMINARY; PRT; 353 AA.
AC O8C1C8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Paraneoplastic ONCONEUROAL protein MAL homolog.
GN PNMAL OR 5730402C15RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).
DR EMBL; AK028331; BAC25885.1; --.
DR MGD; MGI:2180564; Pnmal.
SQ SEQUENCE 353 AA; 39688 MW; 18CEDC3AC4E70939 CRC64;

Query Match 33.9%; Score 822; DB 11; Length 353;
Best Local Similarity 49.4%; Pred. No. 2.2e-57;
Matches 175; Conservative 54; Mismatches 117; Indels 8; Gaps 4;

Qy 1 MPTLLQDWCRCGEHLNTRCMLILGIPDCGDEFEETLQACRHLGRLVGRVGRMFRREE 60
Db 1 MAMTLLDWCRCGMDVNSQRALLVWGIPVNCDETEIETLQAMPQVS--YRVLGRMFWREE 59

Qy 61 NAKAILELAQDIDYALLPREIPGKGGPWEIVKPRNSDGEFLNRLNRLNLEERRTVSDM 120
Db 60 NAKAALDELGTVDYSLIPREMPGKGLWKVFKPTSDAFLRLHLFLAREGWTQDV 119

Qy 121 NRVLGSDTNC SAPRVTISPEFWTWAQTLGAAVQPLLEQMLYRELRFVSGNTISIPGALAF 180
Db 120 ARVLGFQNPAPAPGPEPAEMLVN--ILDNVIQPLVESIWYKLTLPFGKDIIPGGEETF 177

Qy 181 DAWLEHTTEMLQMWQVPEGEKRRRLMECLRGPAQVSLGRASNASITVECLAAQOVF 240
Db 178 DSWLEHSENEIEEQQVSDIEKRRRLMESLRGPAADVIRILKTNPAITTAECLEKALEQV 237

Qy 241 GPVESHKIAQVKLCAYQAEAGEKVSFVLRLPELQRAVENNVSRNNVOTRLKRVLSG 300
Db 238 GSVESSRDAQVRFNTYQNPGEKLSYVIRLEPLQKVVKGIDKONVQARLEQVIAG 297

Qy 301 ATLDPKLRDLKLMKQRRKP--PGFLALVKKLRE---EWEATLGPDRSLEG 349

Db 298 ANHSGALRRQLWLAGAEGPAPNLFOLLVQIREEEAKKEEEAEALLQLGLEG 351

RESULT 11

Q8NG07 PRELIMINARY; PRT; 353 AA.
 AC Q8NG07
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Paraneoplastic antigen.
 GN PNMA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schueller M.M., Jenne D.E., Schutze dit Belkner N., Hohlfield R.,
 RT "Mal (PNMA1).";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Strausberg R.;
 DT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF320308; AAN05100.1; -
 DR EMBL; BC039577; AAN05100.1; -
 SQ SEQUENCE 353 AA; 39761 MW; EB7F5B6AEDA25961 CRC64;

Query Match 33.8%; Score 818; DB 4; Length 353;
 Best Local Similarity 49.6%; Pred. No. 4.5e-57;
 Matches 172; Conservative 52; Mismatches 113; Indels 10; Gaps 4;

QY 1 MPTLLQDWCRCGHLNTRRCMLILGIPEDCGEDEFETQACRHILGRYVIGRMFRREE 60
 DB 1 MAMTLLDWCRCGMDVNSQRLVWGIPIVNCDEAEIETLQAAMPQVS-YRMLGRMFWRREE 59
 QY 61 NQAAILLELAQDIDYALLPREIPGKGPWEIVKPNRSDGFLNRLNRLLEERRTVSDM 120
 DB 60 NAKAALLELTGAVDVAIIPREMPGKGVWVLFKPTSDAEFLERLHLFLAREGWTVDV 119
 QY 121 NRVLGSDTNCSPRVTISPEFTWQTLGAQVPLLEQMLYRELRFVSGNTISIPGALAF 180
 DB 120 ARVLGFQNPPTPGPMPAEMLY--ILDNVIQPLVESIWYKELTLFSGRDIPGGEETF 177
 QY 181 DAWLEHTTLMQWQVPEGEKRRRLMECLRGALQVSGLRASNASITVEECIALAQVVF 240
 DB 178 DPWLEHTNEVLBEWQVSDVEKRRRLMESLRGPAADVIRILKSNPFAITTAECIKALEQVF 237
 QY 241 GPVESHKIAQVLCCKAYQAGKVSFVLRLPLQLQRAVENVVSRNVNTRKRVLSG 300
 DB 238 GSVESSRDAQIKFLNTYQNGEKLQAYVIRLPLQKVKVEKAIDKDNVQARLQVVIAG 297
 QY 301 ATLDPKRLDKLMKQRRKP-PGFLALVKLR-----EEBEWEATL 340
 DB 298 ANHSGAIRRQLWLTGAGEGAPNLFOLLVQIREEEAKKEEEAEATL 344

RESULT 12

O95144 PRELIMINARY; PRT; 353 AA.
 AC O95144
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Paraneoplastic neuronal antigen MAL.
 GN MAL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;

[1]

RN SEQUENCE FROM N.A.
 RP TISSUE=Cerebellum;
 RC MEDLINE=99158179; PubMed=10050892;
 RA Dalmat J., Gultekin S.H., Voltz R., Hoard R., DesChamps T.,
 RA Balmaceda C., Batchelor T., Gerstner E., Eichen J., Frennier J.,
 RA Posner J.B., Rosenfeld M.R.;
 RT "Mal, a novel neuron- and testis-specific protein, is recognized by
 RT the serum of patients with paraneoplastic neurological disorders.";
 RL Brain 122:27-39(1999).
 RN [2]

[2]

RN SEQUENCE FROM N.A.
 RP TISSUE=Cerebellum;
 RC Dalmat J., Rosenfeld M.R., Voltz R., Hoard R.;
 RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF037364; AADI3810.3; -
 DR GO; HGNC:9158; PNMA1.
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0005730; C:nucleolus; TAS.
 DR GO; GO:0007417; P:central nervous system development; TAS.
 DR GO; GO:0007283; P:spermatogenesis; TAS.
 SQ SEQUENCE 353 AA; 39800 MW; 3BB41691AB989AD3D CRC64;

Query Match 33.7%; Score 816; DB 4; Length 353;
 Best Local Similarity 49.6%; Pred. No. 6.5e-57;
 Matches 172; Conservative 52; Mismatches 113; Indels 10; Gaps 4;

QY 1 MPTLLQDWCRCGHLNTRRCMLILGIPEDCGEDEFETQACRHILGRYVIGRMFRREE 60
 DB 1 MAMTLLDWCRCGMDVNSQRLVWGIPIVNCDEAEIETLQAAMPQVS-YRMLGRMFWRREE 59
 QY 61 NQAAILLELAQDIDYALLPREIPGKGPWEIVKPNRSDGFLNRLNRLLEERRTVSDM 120
 DB 60 NAKAALLELTGAVDVAIIPREMPGKGVWVLFKPTSDAEFLERLHLFLAREGWTVDV 119
 QY 121 NRVLGSDTNCSPRVTISPEFTWQTLGAQVPLLEQMLYRELRFVSGNTISIPGALAF 180
 DB 120 ARVLGFQNPPTPGPMPAEMLY--ILDNVIQPLVESIWYKELTLFSGRDIPGGEETF 177
 QY 181 DAWLEHTTLMQWQVPEGEKRRRLMECLRGALQVSGLRASNASITVEECIALAQVVF 240
 DB 178 DPWLEHTNEVLBEWQVSDVEKRRRLMESLRGPAADVIRILKSNPFAITTAECIKALEQVF 237
 QY 241 GPVESHKIAQVLCCKAYQAGKVSFVLRLPLQLQRAVENVVSRNVNTRKRVLSG 300
 DB 238 GSVESSRDAQIKFLNTYQNGEKLQAYVIRLPLQKVKVEKAIDKDNVQARLQVVIAG 297
 QY 301 ATLDPKRLDKLMKQRRKP-PGFLALVKLR-----EEBEWEATL 340
 DB 298 ANHSGAIRRQLWLTGAGEGAPNLFOLLVQIREEEAKKEEEAEATL 344

RESULT 13

Q9BE35 PRELIMINARY; PRT; 150 AA.
 AC Q9BE35
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cerebellum;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

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RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AB060198; BAB41142.1; -.
DR EMBL; AB062932; BAB60727.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 1.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; Znf_C2HC; 1.
DR PROSITE; PS00158; ZF_CCHC; 1.
KW Hypothetical protein_150
SQ SEQUENCE 150 AA; 16756 MW; D842F88B3C8A34A1 CRC64;

Query Match 32.7%; Score 793; DB 6; Length 150;
Best Local Similarity 98.0%; Pred. No. 1.3e-55;
Matches 147; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 314 MKQRKPPGFLALVKLREEWEATLGPDRSLEGLVAPRPPARITGVGAVPLPASGN 373
DB 1 MKQRKPPGFLALVKLREEWEATLGPDRNLEGLVAPRPPARITGVGAVPLPASGN 60

QY 374 SFDARPSQYRRRRGRRGGVARAGSRGSRKRKHTFCYSCGDGHIRVQCINPNSL 433
DB 61 SFDVPPSQYRRRRGRRGGVARAGSRGSRKRKHTFCYSCGDGHIRVQCINPNSL 120

QY 434 LLVQKQKQAAVESGNGNWDKSHPKSKAK 463
DB 121 LLVQKQKQAAVESGNGNWDKSHPKSKAK 150

RESULT 14
Q96BY2 ID Q96BY2 PRELIMINARY; PRT; 351 AA.
AC Q96BY2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Modulator of apoptosis 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC015044; AAH15044.1; -.
DR Genew; HGNC:16658; MOAPL.
SQ SEQUENCE 351 AA; 39512 MW; 5310142AC02B563C CRC64;

Query Match 31.7%; Score 768.5; DB 4; Length 351;
Best Local Similarity 46.6%; Pred. No. 4e-53;
Matches 165; Conservative 60; Mismatches 118; Indels 11; Gaps 6;

QY 1 MPTLLQDWCRCGEHLNTRCMLILGIPDCGDEFEETLQACRHLGRYRVIGRMFRREE 60
DB 1 MTLRLLEDWCRCGMDMNPRAKLLIAGISQSCSVAETEEALQAGLAPLGEYRLIGRMFRDE 60

QY 61 NQAAILLELAQIDYALLPREIPGKGGPWEIVKPRNSDGEFLNRLNRFLEERETVSDM 120
DB 61 NRKVALVGLTARTSHALVPKEIPGKGIWRVIFKPPDPDNTLSRLNEFLAGEGMTVGL 120

QY 121 NRVLGSDTNCSPRVITISPEFT--WAOTLGAAGVPLLEOMLYRELRFVSGNTGISPAL 178
DB 121 SRAUGHENGSLDPEQGMIPEMWAPMLAQAL-EALQPALQCLKYKLRVFSRESPEPGE 179

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QY 179 AFDAWLEHTTEMLQMWQVPEGEKRRRLMECLRGPAQVWGLRASNASITVEECALAQ 238
DB 180 EFGRWPHFTQMIKAWQVPEKRRRLLESRLGPAQVWGLRASNASITVEECALQEE 239

QY 239 VFGPVESSHIAQVKKCKAYQAGEKVSFVLRLEPLQRAVENNVSRNVNQTRLKRVL 298
DB 240 VFGVTDNPRELVQKYLTYTKDEKLSAYVLRLEPLQKLVQGAIBRDVAQNQARLDQV 299

QY 299 SGATLPDKLRDKLKMQRKPPGFLALVKLRE---EEWEATLGPDRSLEG 349
DB 300 AGA-VHKTIRRELNL-PEDGPAFGFLQLLVLIKDYAAEEEEEALL---QALLEG 348

RESULT 15
Q96A40 ID Q96A40 PRELIMINARY; PRT; 399 AA.
AC Q96A40;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ30760.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AK055322; BAB70902.1; -.
DR EMBL; BC007631; AAH07631.1; -.
KW Hypothetical protein.
SQ SEQUENCE 399 AA; 43875 MW; 256F5733C3EBB07D CRC64;

Query Match 31.7%; Score 768.5; DB 4; Length 399;
Best Local Similarity 42.5%; Pred. No. 4.9e-53;
Matches 171; Conservative 72; Mismatches 130; Indels 29; Gaps 7;

QY 1 MPTLLQDWCRCGEHLNTRCMLILGIPDCGDEFEETLQACRHLGRYRVIGRMFRREE 60
DB 1 MAVTMLQDWCRCGWMGNARRGLLIGIPDCDABFQESLEAALRPMGHFTVLGKAFRED 60

QY 61 NQAAILLELAQIDYALLPREIPGKGGPWEIVKPRNSDGEFLNRLNRFLEERETV 118
DB 61 NATAALVELDREYNALVPRPIPGTGPWNVVFVPRCSGEBFLGLGRVHFHPEQGMV 120

QY 119 DMNRVLGSDTNCSPRVITISPEFTWAOTLGAAGVPLLEOMLYRELRFVSGNTGISPAL 178
DB 121 SVAGALG-----VGLRRV-----CWLRISIQAVQVPWEAVRCQSLGVFSGRDQAPGEE 169

QY 179 AFDAWLEHTTEMLQMWQVPEGEKRRRLMECLRGPAQVWGLRASNASITVEECALAQ 237
DB 170 SFEVLDHTTEMLHVMQGVSRERRRRLLEGLRGTLQVHALLAENPARTAQDCCLAA 229

QY 238 QVFGVESHKTAQVKLCHAYQAGEKVSFVLRLEPLQRAVENNVSRNVNQTRLKRV 297
DB 230 QVFGDNEQATIRVKLTAAQQSGERLSAFVLRLEVLQKAMEKALARASADRVLRLQM 289

QY 298 LSGATLPDKLRDKLKMQRKPPGFLALVKLREEWEATLIG----PDRESLEGLEVA 353

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Db 290 LTRAHLEPLDEALRKLRMAGRSPSPLEMLGLVRESEAWESLARSVRAQTQEGAGARAG 349
QY 354 PREPARI-TCVGAVP-----LPASGNSFDARPSQGYR 384
Db 350 AQAVARASTKVEAVPGGPGREPEGLAQAGGQAEELLQEGLK 391

Search completed: September 27, 2004, 17:10:11
Job time : 60.2533 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 17:05:46 ; Search time 20.4265 Seconds
(without alignments)
2180.341 Million cell updates/sec

Title: US-10-037-860-13
Perfect score: 2423
Sequence: 1 MPTLLQDWCGRGHLNTRRC.....VESGNGNNAWDKSHPKSKAK 463

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	5.0	273	2 S00953	gag protein - frui
2	117	4.8	349	2 T18349	probable gag prote
3	117	4.8	1419	2 T32970	hypothetical prote
4	116	4.8	2287	2 T21312	hypothetical prote
5	114.5	4.7	474	2 S28419	lamin B-3 - mouse
6	114.5	4.7	661	2 T37753	hypothetical prote
7	113	4.7	476	2 A95982	probable GTP-bind
8	112.5	4.6	1356	2 F94486	probable retroelem
9	112	4.6	628	2 T23281	hypothetical prote
10	112	4.6	915	2 T26695	hypothetical prote
11	112	4.6	1041	2 T33699	hypothetical prote
12	111	4.6	1335	2 B84512	probable retroelem
13	110.5	4.6	838	2 G84599	probable retroelem
14	110	4.5	373	2 A44478	probable cell grow
15	109	4.5	406	2 E73366	conserved hypothet
16	109	4.5	1272	2 T49313	copia-type reverse
17	109	4.5	1320	2 F96614	probable copia-typ
18	109	4.5	1352	2 F86246	hypothetical prote
19	109	4.5	1352	2 T47925	copia-type polypro
20	109	4.5	2261	2 T20978	hypothetical prote
21	107	4.4	2241	2 T20971	hypothetical prote
22	106.5	4.4	857	2 S33821	median body protei
23	105.5	4.4	813	2 S36018	gene transact-P88
24	105.5	4.4	1864	2 F86378	hypothetical prote
25	105	4.3	759	2 T00153	protein F2109.12 [
26	105	4.3	783	1 A38637	hypothetical prote
27	105	4.3	1260	2 H89984	hypothetical prote
28	105	4.3	1291	2 S02021	micropia polyprote
29	104.5	4.3	627	2 B84482	probable gag-prote

30 104.5 4.3 864 2 B90395
31 104 4.3 483 2 AH3445
32 104 4.3 1508 2 E87696
33 103 4.3 619 2 E82141
34 102.5 4.2 4367 1 B54802
35 102 4.2 200 2 T52627
36 102 4.2 551 2 G95099
37 101.5 4.2 754 2 H84710
38 101.5 4.2 1050 2 JW0092
39 101.5 4.2 1733 1 B45344
40 101 4.2 550 2 A46419
41 100.5 4.1 761 2 H65083
42 100.5 4.1 1008 2 H85055
43 100 4.1 227 2 G71491
44 100 4.1 294 2 D83136
45 100 4.1 859 2 T35785

ALIGNMENTS

RESULT 1

S00953
gag protein - fruit fly (Drosophila melanogaster) transposon 1731
C;Species: Drosophila melanogaster
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jul-2000
C;Accession: S00953
R;Fourcade-Peronnet, F.; d'Auriol, L.; Becker, J.; Galibert, F.; Best-Belpomme, M.
Nucleic Acids Res. 16, 6113-6125, 1988
A;Title: Primary structure and functional organization of Drosophila 1731 retrotransposon
A;Reference number: S00953; MUID:88289356; PMID:2456522
A;Accession: S00953
A;Molecule type: DNA
A;Residues: 1-273 <FOU>
A;Cross-references: EMBL:X07656; NID:g8700; PIDN:CAA30502.1; PID:g8701
C;Genetics:
A;Gene: gag
A;Cross-references: FlyBase:FBgn0000007

Query Match 5.0%; Score 121; DB 2; Length 273;
Best Local Similarity 20.8%; Pred. No. 0.25;
Matches 64; Conservative 52; Mismatches 102; Indels 90; Gaps 15;

Qy 179 AFDALHTTTLQ---MWQVPECEKRRRLMECLRGPALQ-----VVSGLRAS--- 223
Db 14 SYETWSIQMRSLVHACLWKVVSQSVK--PEVDTGGAWOSQDEKALATITLSVKSSQLG 71
Qy 224 --NASITVECLALQOVF--GPVESHKIAQVKLCRAYQAGEKVSFVLRLEPLLQR- 277
Db 72 YVKGCLTAARAWKVLQDVHQPKGLRTVMLYKLLSKELLE-GQSISSHIKEFEIPDAL 130
Qy 278 -AVENNVVSRNNVQTLKRLVSGATLPDKLRDKLKMQRKPPGFLAL-VKLLRBEFE 335
Db 131 DAVEIGITE-----KLSRVLLSSLPSEFNEFWAIETRDDVFLFDALCIKIEEDTR 183
Qy 336 WEATLGPDRSLEGLVA-----PRPARIITGVANVPLPASGNSFDAPSPSGYQRRR 387
Db 184 ---RGAEQQRKQTESAKAFTAVHKPQAPAR-----EAPR----- 216
Qy 388 GRGQHRGGVAVARSGRSRKRKHTFCVSCEDGHIRVQC-----INFSNLLLVKKQKQAA 443
Db 217 -----SAKRDVVCYNGCERHFRANCERKVNKESATQEQCSLLNA 259
Qy 444 VESGNGNW 451
Db 260 LDSG-GFW 266

RESULT 2

T18349
probable gag protein - rice blast fungus gypsy retroelement
C;Species: Magnaporthe grisea (rice blast fungus)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000


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Qy 378 RPSQGVRRRRGRQ 391
Db 291 -PAKEHEILGEQ 303

RESULT 5
S28419
lamin B-3 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Jun-2000
C:Accession: S28419
R:Furukawa, K.; Hotta, Y.
EMBO J. 12, 97-106, 1993
A:Title: cDNA cloning of a germ cell specific lamin B(3) from mouse spermatocytes and an
A:Reference number: S28419; MUID:93154351; PMID:8094052
A:Accession: S28419
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-474 <FUR>
A:Cross-references: EMBL:D13455; NID:g220471; PIDN:BAA02708.1; PID:g220472
C:Superfamily: cytoskeletal keratin

Query Match 4.7%; Score 114.5; DB 2; Length 474;
Best Local Similarity 23.9%; Pred. No. 1.5;
Matches 86; Conservative 48; Mismatches 147; Indels 79; Gaps 18;

Qy 145 AQTILGAAVQPLLEQMLYRELRFV-----SGNT-----ISIPGALAFD-AWLEHTTTEML 191
Db 22 ARPLMETVEGALPELRGRLREYVYKRGPGIGKTPVEDPVKSEGAAGVYPTWNNHLRVPT 81

Qy 192 QMNOVPEGEKR--RRIMECLRGALQVVGSLGRASNASITVECLAA-----QQV-RGPV 243
Db 82 REQEVRETRRRHRLVE-----VDSRQOEYDFKMAQALEDLRSQHDQVRLYRV 132

Qy 244 ESHKIAQVGL-----CKAYQAGEKVSFVLRLPL-----LQR---AVENNIV 284
Db 133 ELETQYQAKLUNAKLSDNDKAHAAREEKEARMRVESLSYQLLGKQKQASAEHHI- 191

Qy 285 SRRNVNQTLRKRVLSGATLPDKLRKLMQRRKPPGFLALVLRREEEWEATLQPD- 343
Db 192 -----HELEALAGER--DKFRKMLDAKQEMTEVRDAMQQLAEYOELLDIKALDM 242

Qy 344 -----RESLEG-----LEVAPPPARITGVAVPLPASGNSFDARPSQY-RRRRGRGQHR 393
Db 243 EISAYRKLLEGEERLKLSPSPSRITTSRATSSSSSGVMGSGQGRGRRLTETDT 302

Qy 394 RGGVARAG--SRGSRKRRHTFCYSGEDGHRVQCINPNSLLLVKQKQAAVESGNGW 451
Db 303 SGSPSRASRVSGSRLAQTV-----ATGVVNIDEVDPEG-RFVRLKNSSDKQOSLGNW 355

RESULT 6
T37753
hypochemical protein SPAC1687.10 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T37753
R:Wedler, H.; Wambutt, R.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, December 1998
A:Reference number: Z21744
A:Accession: T37753
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-661 <WED>
A:Cross-references: EMBL:AL035064; PIDN:CAA22604.1; GSPDB:GN00066; SPDB:SPAC1687.10
A:Experimental source: strain 972h; cosmid c1687
C:Genetics:
A:Gene: SPDB:SPAC1687.10
A:Map position: 1
A:Introns: 248/3

Query Match 4.7%; Score 114.5; DB 2; Length 661;
Best Local Similarity 21.5%; Pred. No. 2.3;

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Matches 68; Conservative 35; Mismatches 131; Indels 83; Gaps 11;

Qy 100 GFELNRLNPLEERRTVSDMR--VLGSDTNCAPRTVISPEFWTWAQTLGAQVQLLE 157
Db 324 GELNNMIRRYLLESRVYKESQRMKVL-----GSASQPFLL 360

Qy 158 QMLYRELRFVSGNTISIPGALAFDAMLEHTTEMLQMOVPEGEKRRRLMECLRGPALQV 217
Db 361 KRLOKDFQLLAKLI-----CALREWEEDNEKKIYVFGKPLSS---RLLMHSPILQNG 412

Qy 218 SGLRASNASITVECLAAALQOVFGPVESHKIAQVVKLCAYQAGEKVSFVLRL-----EP 273
Db 413 ENISSNDNSKSPESPAPKTTGKIENKKLRNDV-----QSKKSIRFPRLRLASHEEP 466

Qy 274 LLQRAVENNVVSRNVNQTLRKRVLSGATLPDKLRKLMQRRKPPGFLALVLRREE 333
Db 467 LIDRMVNQSPDTRSVSKSKRLVRETSSGCL-FKNHKSNTLSPPRKG-----SRH 515

Qy 334 EWEATLQPD-----RESLEGLVAPRPPARITGVGAVP----- 367
Db 516 GPREPCUSPDASSSSIPVTDIKEILPSQHDTPHNSVKLTGSSITTPASVSLRQMIPLLSR 575

Qy 368 LPASG---NSFDARPSQ 381
Db 576 TPPKGEEFTNSLDDTPTQ 592

RESULT 7
A95982
probable GNP-binding protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmi
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: A95982
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan-
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo-
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: A95982
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-476 <KUR>
A:Cross-references: GB:AL591985; PIDN:CAC49521.1; PID:g15141008; GSPDB:GN00167
A:Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hehault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: engA; SMb20995
A:Genome: Plasmid
C:Superfamily: Mycobacterium leprae probable GTP-binding protein; translation elongation

Query Match 4.7%; Score 113; DB 2; Length 476;
Best Local Similarity 23.7%; Pred. No. 1.9;
Matches 88; Conservative 41; Mismatches 101; Indels 142; Gaps 24;

Qy 80 REIFPGK-----GPWEIVKPRNSDGEFLNRLNRELEERRTVSDMRVLGS 126
Db 183 RPAVEGEGTEDEVEPAYDETPLRVAIVGRPNACK-STLINRFLGEDR-----LIT 232

Qy 127 DTNCSAPRTVISPEFWTWA-----OTLG-----AAVQPLLEOM-----LYRELRFVSGNT 171
Db 233 GPEAGITRDSISVE-WDWRGRTIKMFDTAGRRKAKVQEKLEKLSVADALRAIR-FAETV 290

Qy 172 I-----SIP-----GALAFDAWLEHTTEMLQMWQ---VPEGEKRRRL 205
Db 291 VIVFDATIPFEKQDLQIVDLVLRGAAVLAFAFKW-----DLVENWQALLDLREKTERL 345

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Db 310 KENVESFERVEKLV--AMTSGKSIDYIQSTALHTFLEG-----LGDHIQWEVKAK 361
 QY 319 KPFGFLALVKLREEEWEATLQPD-----RESLEGLVAPRPAPRITGVGAVPLPAS 371
 Db 362 RP-----LTLEAYDALSOELLQDKMRKQIED-----PVA----- 393
 QY 372 GNSFDARPSGQRRRRGQRRGGVARAGSRKRKHTFCYSCGEDGHRVQCINPS 431
 Db 394 -NAFFAR-----HGLQKNSFVGNCCYCGKRGHTANEC----- 424
 QY 432 NLLLVKQKQAAVESGNG 449
 Db 425 -----RRKKSDESQNG 435

RESULT 11
 hypothetical protein F49F1.8 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T33699
 R:Miller, N.; Wamsley, P.
 submitted to the EMBL Data Library, October 1998
 A:Description: The sequence of C. elegans cosmid F49F1.
 A:Reference number: Z21389
 A:Accession: T33699
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1041<MIL>
 A:Cross-references: EMBL:AF100656; PIDN:AAC68951.1; GSPDB:GN00022; CESP:F49F1.8
 A:Experimental source: strain Bristol N2; clone F49F1
 C:Genetics:
 A:Gene: CESP:F49F1.8
 A:Map position: 4
 A:Introns: 172/3; 293/1; 334/3; 579/1

Query Match 4.6%; Score 112; DB 2; Length 1041;
 Best Local Similarity 22.0%; Pred. No. 6.5;
 Matches 56; Conservative 50; Mismatches 88; Indels 60; Gaps 12;

QY 84 GKGGPWEIVKPRNSDGEFLNRLNLFLEERR-----TVSP----- 119
 Db 777 GEGGELDVAVRTQSKVLETRDILERSNVASATPPSTASDGAGSTFEENVIOQVAQ 836
 QY 120 ----MNRVLG-----SDTNCAPRTVTSPEFWTAQTLGAAV-----QPLLEQWLY 161
 Db 837 ANQGSSEMGQSVNSDSDTNAAPLSVAVDKK---RSGSVGNKSKSYEDRPILGMLRL 893
 QY 162 R---ELRVSGNTISIPCALAFDAWLEHTTMLQWQ-VPEGEKRRRLMECLRGPALQVV 217
 Db 894 RPAVLQTFYKGTM-----AEDFSFIRSFKDQCEASEKLTDDQLKFLTCLLDRARNA 948
 QY 218 SGLRASNASITVECLAAQOVF-GPV-ESHKIAQVKCKAYQAGEKVSFVLRLPL 275
 Db 949 EDETKLNAVTEGLIARMTTFENPVLIKHNQLRLCK--QXPERSVEAFHLRIELE 1006
 QY 276 QRA--VENNVVSR 287
 Db 1007 RAASTVENIVTKR 1020

RESULT 12
 B84512
 Probable retroelement pol polyprotein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C:Accession: B84512
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: B84512
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1335<STO>
 A:Cross-references: GB:AE002093; NID:g4388818; PIDN:AAD19773.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g13930
 A:Map position: 2
 C:Superfamily: retrovirus-related polyprotein

Query Match 4.6%; Score 111; DB 2; Length 1335;
 Best Local Similarity 18.8%; Pred. No. 11;
 Matches 59; Conservative 42; Mismatches 104; Indels 108; Gaps 11;

QY 197 PEGEKRRRLMECLRGPALQVVSGLRASNASITVECLAAQOVFGPVESHKIAQVKCKA 256
 Db 29 PEKRRKRDADAVAR-----LERCDKAKNVIFLNVDKVLAKIELCKT 70
 QY 257 YQAGEKVSFVRLRP-----LLQRAVENNV-----VSRNVNQT 292
 Db 71 AAFAWETDLRFMRSLPHRVYTQLSFYTPKMQENKKIDENIDFLKIVADLAHLQIDVT 130
 QY 293 -RLKRVLSGATLP---DKLRDKLKMQRKPPGFLALVKLLREEEWEATLGPDRSLE 348
 Db 131 DEVOAILLLSSLPARYDGLVETWKYSNRK-----LRLDDVMVAARDKERE--- 177
 QY 349 GLEVAPRPAPRITGVGAVPLPAGNSFDARPSQYRRRRGQRRGGVARAGSRKR 408
 Db 178 -LSQNNRP-----VVEGHFARGPRPDGNNQGNKGNKRSKSGADGR----- 219
 QY 409 KRHTFCYSCGEDGHRVQC-----INPSNLLLVKQKKQ 441
 Db 220 ----VCWICGEGHFKQCYKWIERNKSKQSGSDNGESSLAKSTEAFNPAMVLLATDTL 275
 QY 442 AAVESGNGNNAWD 454
 Db 276 VVTDSIANEWVLD 288

RESULT 13

G84599
 Probable retroelement pol polyprotein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: G84599
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: G84599
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-838<STO>
 A:Cross-references: GB:AE002093; NID:g4567266; PIDN:AAD23679.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g21310
 A:Map position: 2

Query Match 4.6%; Score 110.5; DB 2; Length 838;
 Best Local Similarity 21.1%; Pred. No. 6.2;
 Matches 61; Conservative 49; Mismatches 120; Indels 59; Gaps 10;

QY 214 LQVVSGLRASNASITVECLAAQOVFGPVESHKIAQVKCKAYQAGEKVSFVLRL--- 270
 Db 31 LGLLEGLEDEEA-JEEESTETDTSILTKTED-KVLEKRCARSTVLSLGNHVLKVI 88
 QY 271 ---LEPLLQRAVENNVSRNVNQTRLKRVLSG-----ATLPDKLRDKLKLKMKORR--- 318
 Db 89 KEKTAAGMIRVLDFLKFMAKSLPNRIYLKORLYGYKMSDSMTIEENVNDFFKLISLENVK 148

QY 319 -----KPPGFLALVKLREEEWEATLGPDRSLEGLVAPRPAITGVGAVPLPASG- 372
 Db 149 VSPBEDQAIULMSLPKQFDQKTLKYKTKTLALDEITGAIRSKVLELG-----ASGK 203
 QY 373 ---NSFDARPSOYRRRRRGHRRGGVARGSRGSRKRKRTHTFCYSCGEDGHIRVQCIT- 428
 Db 204 MLKNSDAL---FVQDRGRSEKDKSSERNKSQSRKSKREKKVCVWCCKEGHFKQCYV 259
 QY 429 -----NPSNT-----LLVQKQQAQAVESGNGNWAWD 454
 Db 260 WKEKNKGNNSKGGSSNVIGQAAADAAALAVRESNADNQVDNEWIMD 308
 RESULT 14
 A44478
 probable cell growth or differentiation regulator (alternatively spliced type I transcrip
 C:Species: Homo sapiens (man)
 C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C:Accession: A44478
 R:Weitzel, J.N.; Kasperczyk, A.; Mohan, C.; Krontiris, T.G.
 Genomics 14, 309-319, 1992
 A>Title: The HRAS1 gene cluster: two upstream regions recognizing transcripts and a third
 A:Reference number: A44478; MUID:93052330; PMID:1339391
 A:Accession: A44478
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-373 <WEI>
 A:Cross-references: GB:M91083; NID:g184389; PIDN:AAAS8667.1; PID:g184390
 A>Note: sequence extracted from NCBI backbone (NCBIP:117869)
 Query Match 4.5%; Score 110; DB 2; Length 373;
 Best Local Similarity 24.2%; Pred. No. 2.3;
 Matches 97; Conservative 49; Mismatches 144; Indels 110; Gaps 20;
 QY 22 LILGTPDCGEDBEFTLQEAACHHGRVYVIGRMFRRE-----NAQAIILELAQD 72
 Db 20 VVCGVSEQTTCEWVIALAQAIQTGRFVLQVRLREKERQLLPQECPVGAQATCGQFASD 79
 QY 73 IDYALLPREIPKGG-----PWE-----VVKPNSDGEFLNRLNRLREERRTV 117
 Db 80 VQF-VLVRTGPSLAGRPSSDCPPPERCLIRASLPVKPPAALG-----CBPRKTL 128
 QY 118 SMNRLVSGDITNCSAPRVTISPEFTWAQTLGAAVQPLLEQMLYRELRFVSGNTISIPGA 177
 Db 129 TPEAPSLSRPGPAAP-VPTPGCCITDLGLRLVQRNAEL-----GH 171
 QY 178 LAFDAWLEHTTLMQWQVPEGEKRRRLMECLRGALQVVSGLRASNA---SITVECLIA 234
 Db 172 EAF--W---EQELRREQAREGQARL-QALSAATAEHAARLQALDAQARALEAELQLA 224
 QY 235 ALQQVFGP-----VESHKIAQVK---LCKAYQAGEKVSFVLRLLEPL 274
 Db 225 A--EAPGPPSPMASATERLHQDLAVQERQSAEVQSSALVSRALAEARA-----LQAQ 276
 QY 275 LQRAVENNVSRNRNQTRLKRVL--SGATLPDKLRDKLMKQRRKPPGFIALVKLLRE 332
 Db 277 AQELEELN---RELRCQNLQQFIQQTGAALPPPRPD-----RGPPTQGLPPARE 325
 QY 333 EEWATLGPDRSLEGLVAPR---PPARITGVGAVPLP 369
 Db 326 ----ESLLGAPGESHAGAPRPRGGPHDAELLEVAAAPAP 361

RESULT 15
 E72366
 conserved hypothetical protein - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: E72366
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
 Nature 399, 323-329, 1999

A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
 A:Reference number: A72200; MUID:99287316; PMID:10360571
 A:Accession: E72366
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-406 <ARN>
 A:Cross-references: GB:AE001728; GB:AE000512; NID:g4981027; PIDN:AAD35612.1; PID:g498104
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gens: TM0527
 C:Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
 F:187-309/Domain: translation elongation factor Tu homology <TU>

Query Match 4.5%; Score 109; DB 2; Length 406;
 Best Local Similarity 22.6%; Pred. No. 3;
 Matches 83; Conservative 56; Mismatches 111; Indels 118; Gaps 19;
 QY 46 LGRYVIGRMFRREENAQAIILELAQDIDYALLPREIP---GKG-----GFW 89
 Db 90 LQRTQVILEIFARHATSEBGLQ---VEMASLLYELPRLVKGGEELSRLGGIGTRPG 145
 QY 90 EVIVP-----RNSDGEFLNRLNRLREERRTVSDMN-----RVLGSNTNCSAP--- 133
 Db 146 EPLLEVLRRHIKNRIQAQLRKRLKE-IEQERNQKQRLKKIPHVSIVGY-TNAGKSTLL 203
 QY 134 RVTISPEFTWAQTLGAAVQPLLEQMLYRELRFVSGNTISIPGALAFDAWLEHTTLMQ 193
 Db 204 KYLTSDVTV-ADKLFATLEPVT---RRLKLSGRVILVSDTVGFIKLEPHT----- 251
 QY 194 MQVPEGEKRRRLMECLRGALQVVSGLRASNASIT-----VVECLAALQ 238
 Db 252 -----IVSAFKATLEEIKYSDVLIHLVDASDPYLBKMKASEK 289
 QY 239 VEGPVESHKIA-----QVKLCK-----AYQAGEKVSFVLRLPLEQRAVENNV 283
 Db 290 VLEEIGADKIPRIIVENKIDLCPRERIETLKWKYPEALFISAEKRIQLDLDRLEE--V 347
 QY 284 VSRRNVNQTRLKRVLSGATLPDKLRDKLMKQRRKPPGFALVKLLREBEWEATLGP 343
 Db 348 ISQRDVQET-LKVPLEKIGQIYALKDRUEILNEDYR-EGY-ALI-----TLKTD 393
 QY 344 RESLEGLE 351
 Db 394 RETLEWLX 401

Search completed: September 27, 2004, 17:10:45
 Job time : 23.4265 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 17:10:17 ; Search time 134.663 Seconds
(without alignments)
1105.584 Million cell updates/sec

Title: US-10-037-860-13

Perfect score: 2423

Sequence: 1 MPTLLQDWCRGEHLNTRRC.....VESGNGNWDKSHPKSKAK 463

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1349238 seqs, 321558718 residues

Total number of hits satisfying chosen parameters: 1349238

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2423	100.0	463	13	US-10-037-860-13
2	893.5	36.5	452	16	US-10-037-860-13
3	818	33.8	353	9	US-09-965-529-7
4	818	33.8	353	10	US-09-969-680A-7
5	768.5	31.7	351	9	US-09-965-529-1
6	768.5	31.7	351	10	US-09-969-680A-1
7	768.5	31.7	351	12	US-09-804-014A-16
8	768.5	31.7	351	15	US-10-341-434-10
9	768.5	31.7	351	15	US-10-094-749-1978
10	766.5	31.6	329	13	US-10-037-860-4
11	765.5	31.6	329	12	US-10-037-860-4
12	742	30.6	321	12	US-09-804-014A-39
13	740.5	30.6	312	12	US-09-804-014A-73
14	740.5	30.6	312	12	US-09-804-014A-74
15	618.5	25.5	283	13	US-10-037-860-11

16	462.5	19.1	195	13	US-10-037-860-7	Sequence 7, Appli
17	423.5	17.5	403	15	US-10-094-466-38	Sequence 38, Appl
18	384.5	15.9	337	12	US-10-296-115-1208	Sequence 1208, Ap
19	332	13.7	120	12	US-09-804-014A-42	Sequence 42, Appl
20	324	13.4	120	12	US-09-804-014A-41	Sequence 41, Appl
21	323	13.3	149	13	US-10-037-860-9	Sequence 9, Appli
22	322	13.3	204	14	US-10-029-386-33747	Sequence 33747, A
23	270	11.1	116	9	US-09-864-761-34645	Sequence 34645, A
24	191	7.9	538	16	US-10-408-765A-2992	Sequence 2992, Ap
25	158.5	6.5	1332	15	US-10-374-780A-1037	Sequence 1037, Ap
26	156	6.4	1394	16	US-10-437-963-185722	Sequence 185722,
27	156	6.4	1433	15	US-10-374-780A-1040	Sequence 1040, Ap
28	156	6.4	1433	16	US-10-437-963-110685	Sequence 110685,
29	156	6.4	1828	16	US-10-437-963-123225	Sequence 123225,
30	155.5	6.4	1150	16	US-10-437-963-122585	Sequence 122585,
31	155	6.4	584	12	US-10-221-278-355	Sequence 355, App
32	155	6.4	584	15	US-10-291-172-355	Sequence 355, App
33	154	6.4	1360	16	US-10-437-963-185720	Sequence 185720,
34	154	6.4	2003	16	US-10-437-963-117298	Sequence 117298,
35	152	6.3	1433	15	US-10-374-780A-1035	Sequence 1035, Ap
36	152	6.3	1696	16	US-10-437-963-117296	Sequence 117296,
37	151	6.2	1636	16	US-10-437-963-122665	Sequence 122665,
38	151	6.2	1695	16	US-10-437-963-122632	Sequence 122632,
39	149	6.1	1711	16	US-10-437-963-199076	Sequence 199076,
40	149	6.1	3783	16	US-10-437-963-146318	Sequence 146318,
41	148	6.1	1777	16	US-10-437-963-122620	Sequence 122620,
42	148	6.1	2155	16	US-10-437-963-146341	Sequence 146341,
43	147	6.1	1236	16	US-10-437-963-122619	Sequence 122619,
44	147	6.1	2664	16	US-10-437-963-117303	Sequence 117303,
45	146.5	6.0	1008	16	US-10-437-963-184092	Sequence 184092,

ALIGNMENTS

RESULT 1

US-10-037-860-13
; Sequence 13, Application US/10037860
; Publication No. US2002012114A1
; GENERAL INFORMATION:
; APPLICANT: Jerome B. Posner
; APPLICANT: Josep O. Dalmau
; APPLICANT: Myrna R. Rosenfeld
; TITLE OF INVENTION: Ma FAMILY POLYPEPTIDES AND ANTI-Ma
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 2581.1004-004
; CURRENT APPLICATION NUMBER: US/10/037,860
; CURRENT FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 09/189,527
; PRIOR FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 463
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-037-860-13

Query Match	100.0%	Score 2423;	DB 13;	Length 463;
Best Local Similarity	100.0%;	Pred. No. 6.6e-220;		
Matches 463;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MPTLLQDWCRGEHLNTRRCMLILGIPEDCGEDEFETLQACRHLGRYVIGMFREE	60	
Db	1	MPTLLQDWCRGEHLNTRRCMLILGIPEDCGEDEFETLQACRHLGRYVIGMFREE	60	
Qy	61	NAQAIILEAQIDYALLPREIPCKGGPWEVIVPRNSDGEFLNRLNRFLEERTVSDM	120	
Db	61	NAQAIILEAQIDYALLPREIPCKGGPWEVIVPRNSDGEFLNRLNRFLEERTVSDM	120	
Qy	121	NRVLGSDTNCAPRTVISPEFWTWAQTIGAAVQPLLEQMLYRELRFVSGNTISIPGALAF	180	
Db	121	NRVLGSDTNCAPRTVISPEFWTWAQTIGAAVQPLLEQMLYRELRFVSGNTISIPGALAF	180	


```
; Sequence 7, Application US/09969680A
; Publication No. US20030124649A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti; YUE, Henry
; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731-1 USA
; CURRENT APPLICATION NUMBER: US/09/969,680A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US00/22315
; PRIOR FILING DATE: 2000-08-14
; PRIOR FILING DATE: 1999-08-17
; PRIOR FILING DATE: 1999-08-17
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124649A1 2483172CD1
US-09-969-680A-7

Query Match      33.8%; Score 818; DB 10; Length 353;
Best Local Similarity 49.6%; Pred. No. 2.4e-68;
Matches 172; Conservative 52; Mismatches 113; Indels 10; Gaps 4;

QY 1 MPTLLQDWCRCGEHLNTRRCMLILGIPDCGDEFEETLQACRHGLGRYRVIGRMFRREE 60
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MAMTLLEDWCRCMDVNSQRAALLVWGIPVNCDEABIEETLQAAMPQVS-YRMLGRMFWR 59
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 61 NQAAILLELAQDIDYALLPREIPGKGGPWEIVKPRNSDGEFLNRLNRFLEERRTVSDM 120
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 60 NAKAALLETGAVDYAATPREMPGKGGVKKVLFKPTSDAEFLERLHLFLAREGWTQDV 119
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 121 NRVLGSDTNC SAPRTVISPEPTWAQTLGAAVQPLLEQMLYRELVRVSGNTISIPGALAF 180
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 120 ARVLGFGNQPTTPGPEMAELNY--ILDNVIQLVESIWYKRLTFLSGRDIPOGGETF 177
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 181 DAWLEHTEMLQMWQVPEGEKRRRLMECLRGPAALQVVSGLRASNASITVEECLAALQOVF 240
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 178 DPMLEHTEMLQMWQVSDVPEKRRRLMESLRGPAADVIRILKSNPNPAITTAECLEKALQOVF 237
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 241 GFVESHKIAQVKLCKAYQAGEKVSFVLRLEPLLQRAVENNVSRNNVQTRLRKRVLSG 300
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 238 GSVSSRDAQIKFLNTYQNPQEKLSAYVIRLEPLLQKVKVEKGAIDKONVQARLEQVIAG 297
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 301 ATLPDKLRDLKLMKQRRKP-PGFLALVKKLR-----EEWEATL 340
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 298 ANHSGAIRRQLWLTGAGEGPAPNLFQLLVQIRREAEKEEAEATL 344
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 5
US-09-965-529-1
; Sequence 1, Application US/09965529
; Publication No. US20020182671A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
```

```
; FILE REFERENCE: PF-0731 USA
; CURRENT APPLICATION NUMBER: US/09/965,529
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 112301CD1
US-09-965-529-1

Query Match      31.7%; Score 768.5; DB 9; Length 351;
Best Local Similarity 46.6%; Pred. No. 1.1e-63;
Matches 165; Conservative 60; Mismatches 118; Indels 11; Gaps 6;

QY 1 MPTLLQDWCRCGEHLNTRRCMLILGIPDCGDEFEETLQACRHGLGRYRVIGRMFRREE 60
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MTLRLLEDWCRCMDMNPRAKLLIAGISQSCVAIEEALQAGLAPLGEYRLLRGMRERDE 60
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 61 NQAAILLELAQDIDYALLPREIPGKGGPWEIVKPRNSDGEFLNRLNRFLEERRTVSDM 120
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 NRKVALVGLTAETSHALVPKEIPKGGIMRVIPKPPDPDNTFLSRLNEFLAGEGWTGEL 120
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 121 NRVLGSDTNC SAPRTVISPEFT--WAQTLGAAVQPLLEQMLYRELVRVSGNTISIPGAL 178
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 SRALGHENGSLDPEQGMIPEMWAPMLAAL-EALQPALQCLKYKKLAVFSGRESPEEGEE 179
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 179 AFDWLEHTEMLQMWQVPEGEKRRRLMECLRGPAALQVVSGLRASNASITVEECLAALQ 238
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 180 EFGWMFHHTQMIKAWQVDPVEKRRRLLESIRGPAADVIRILKNNPLITVDECLALEE 239
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 239 VFGVESHKIAQVKLCKAYQAGEKVSFVLRLEPLLQRAVENNVSRNNVQTRLRKRVL 298
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 240 VFGVTDNPRELQVKLTYYQKDEKLSAYVIRLEPLLQKLVQRCIAIERDAVNQARLQVI 299
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 299 SGATPLPKLRDLKLMKQRRKPPGFLALVKKLR---EEWEATLGPDRSLEG 349
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 300 AGA-VHKTIRRELNL-PEDGPAPGFLQLLVLIKDYEAABEEALL---QAILEG 348
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 6
US-09-969-680A-1
; Sequence 1, Application US/09969680A
; Publication No. US20030124649A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti; YUE, Henry
; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731-1 USA
; CURRENT APPLICATION NUMBER: US/09/969,680A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US00/22315
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/149,641
; PRIOR FILING DATE: 1999-08-17
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
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OTHER INFORMATION: Incyte ID No. US20030124649A1 112301C0D1
US-09-969-680A-1

Query Match 31.7%; Score 768.5; DB 10; Length 351;
Best Local Similarity 46.6%; Pred. No. 1.1e-63;
Matches 165; Conservative 60; Mismatches 118; Indels 11; Gaps 6;

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QY 1 MPTLLQDWCRCGHEHNTNRCMLILGIPEDCGDEFEETLQEAACHLGRYRVIGRMFRDE 60
Db 1 MTRLLEDWCRGDMNPRKALLIAGISQSCSVAIEEALQAGLAPLGEYKLLGRMFRDE 60

QY 61 NQAAILLELAQDIDYALLPREIPGKGPWEVIVKPRNSDGEFLNRLNRFLEERRTVSDM 120
Db 61 NRKVALVGLTAETSHALVPKEIPGKGIWRVIFKPPDPDNTFLSRLNEFLAGEMTVGEL 120

QY 121 NRVLGSDTNCSPRVITISPEFWT--WAQTLGAAVQPLLSQMLYRELRFVSGNTISIPGAL 178
Db 121 SRALGHENGLDPEQGMIPEMWAPMLAQAAL-EALQPALQCLKYKLRVFSGRSPFGE 179

QY 179 AFDWLEHTTEMLOMWOVPEGEKRRRLMECLRGPAQOVVSGLRASNASITVEECALAOQ 238
Db 180 EFGRWMEHTTQMKAWQVDPVEKRRRLLESRLGPAQVIRVLIKNNPLITVDECLQALEE 239

QY 239 VFGPVESHKIAQVKLCCKAYQEAQEKVSVFLRLEPLLQRAVENNVVSRNNVQTRKRVL 298
Db 240 VFGVTDNPRELQVKYLTYYQDEEKL SAVVLRLEPLLQKLVQGAERDAVNAQRLDQVI 299

QY 299 SGATLPDKLRDKLKMQRKPPGFALIVKLLRE---EEWEATLGPDRSLEG 349
Db 300 AGA-VHKTIRRELNL-PEDGPAPGFLQLLVLIKDYEAABEEBALL---QAILEG 348
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RESULT 7

US-09-804-014A-16
; Sequence 16, Application US/09804014A
; Publication No. US20030064489A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Vernet, Corine
; APPLICANT: Ferrandes, Elma
; APPLICANT: Shinkets, Richard
; APPLICANT: Spaderina, Steven
; APPLICANT: Majumder, Kumud
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-721 US
; CURRENT APPLICATION NUMBER: US/09/804,014A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/188,316
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/188,277
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/189,139
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: 60/189,140
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: 60/190,401
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/190,231
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-014A-16

Query Match 31.7%; Score 768.5; DB 12; Length 351;
Best Local Similarity 46.6%; Pred. No. 1.1e-63;
Matches 165; Conservative 60; Mismatches 118; Indels 11; Gaps 6;

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QY 1 MPTLLQDWCRCGHEHNTNRCMLILGIPEDCGDEFEETLQEAACHLGRYRVIGRMFRDE 60
```

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Db 1 MTRLLEDWCRGDMNPRKALLIAGISQSCSVAIEEALQAGLAPLGEYKLLGRMFRDE 60

QY 61 NQAAILLELAQDIDYALLPREIPGKGPWEVIVKPRNSDGEFLNRLNRFLEERRTVSDM 120
Db 61 NRKVALVGLTAETSHALVPKEIPGKGIWRVIFKPPDPDNTFLSRLNEFLAGEMTVGEL 120

QY 121 NRVLGSDTNCSPRVITISPEFWT--WAQTLGAAVQPLLSQMLYRELRFVSGNTISIPGAL 178
Db 121 SRALGHENGLDPEQGMIPEMWAPMLAQAAL-EALQPALQCLKYKLRVFSGRSPFGE 179

QY 179 AFDWLEHTTEMLOMWOVPEGEKRRRLMECLRGPAQOVVSGLRASNASITVEECALAOQ 238
Db 180 EFGRWMEHTTQMKAWQVDPVEKRRRLLESRLGPAQVIRVLIKNNPLITVDECLQALEE 239

QY 239 VFGPVESHKIAQVKLCCKAYQEAQEKVSVFLRLEPLLQRAVENNVVSRNNVQTRKRVL 298
Db 240 VFGVTDNPRELQVKYLTYYQDEEKL SAVVLRLEPLLQKLVQGAERDAVNAQRLDQVI 299

QY 299 SGATLPDKLRDKLKMQRKPPGFALIVKLLRE---EEWEATLGPDRSLEG 349
Db 300 AGA-VHKTIRRELNL-PEDGPAPGFLQLLVLIKDYEAABEEBALL---QAILEG 348
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RESULT 8

US-10-341-434-10
; Sequence 10, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-341-434-10

Query Match 31.7%; Score 768.5; DB 15; Length 351;
Best Local Similarity 46.6%; Pred. No. 1.1e-63;
Matches 165; Conservative 60; Mismatches 118; Indels 11; Gaps 6;

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QY 1 MPTLLQDWCRCGHEHNTNRCMLILGIPEDCGDEFEETLQEAACHLGRYRVIGRMFRDE 60
Db 1 MTRLLEDWCRGDMNPRKALLIAGISQSCSVAIEEALQAGLAPLGEYKLLGRMFRDE 60

QY 61 NQAAILLELAQDIDYALLPREIPGKGPWEVIVKPRNSDGEFLNRLNRFLEERRTVSDM 120
Db 61 NRKVALVGLTAETSHALVPKEIPGKGIWRVIFKPPDPDNTFLSRLNEFLAGEMTVGEL 120

QY 121 NRVLGSDTNCSPRVITISPEFWT--WAQTLGAAVQPLLSQMLYRELRFVSGNTISIPGAL 178
Db 121 SRALGHENGLDPEQGMIPEMWAPMLAQAAL-EALQPALQCLKYKLRVFSGRSPFGE 179

QY 179 AFDWLEHTTEMLOMWOVPEGEKRRRLMECLRGPAQOVVSGLRASNASITVEECALAOQ 238
Db 180 EFGRWMEHTTQMKAWQVDPVEKRRRLLESRLGPAQVIRVLIKNNPLITVDECLQALEE 239

QY 239 VFGPVESHKIAQVKLCCKAYQEAQEKVSVFLRLEPLLQRAVENNVVSRNNVQTRKRVL 298
Db 240 VFGVTDNPRELQVKYLTYYQDEEKL SAVVLRLEPLLQKLVQGAERDAVNAQRLDQVI 299

QY 299 SGATLPDKLRDKLKMQRKPPGFALIVKLLRE---EEWEATLGPDRSLEG 349
Db 300 AGA-VHKTIRRELNL-PEDGPAPGFLQLLVLIKDYEAABEEBALL---QAILEG 348
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RESULT 9
US-10-094-749-1978
; Sequence 1978, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; PRIOR FILING DATE: 2002-03-12
; PRIOR FILING DATE: 2002-01-24
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1978
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-1978

Query Match      31.7%; Score 768.5; DB 15; Length 399;
Best Local Similarity 42.5%; Pred. No. 1.4e-63;
Matches 171; Conservative 72; Mismatches 130; Indels 29; Gaps 7;

Qy      1  MPTLLQDWCRCGEHLNTRRCMLILGIPEDCCGDEBFEETLQACRHLGRYRVIQRMFRREE 60
Db      1  MAVTMLQDWCRCWGMGNARRGLLILGIPEDCCDAAEFQESLEAALRPMGHFTVLGKAFREED 60

Qy      61  NQAAILLELAQDIDYALLPREIPKGGPWEVIVKPRNSDGEF--LNRLNRFLEERRTVS 118
Db      61  NATAAVELDREVNVALVPREIPGTGPNVNVFVPRCSGEEFLGLGRVFFHPEQEQWVE 120

Qy      119  DMNRVLGSDTNCSPRVTTISPEFTWTAQTLGAAVQPLLEQMLYRELRFVSGNTISIPGAL 178
Db      121  SVAGALG----VGLRRV-----CWLRSIQAVQVPWEAVRCOSLGVFSGRDQAPGEE 169

Qy      179  AFDALWHTTEMLQMWQ-VPEGEKRRRLMECLRGPALQVVSGLRASNASITVBECLAALQ 237
Db      170  SFEVLDHTTEMLHWQGVSRERRRLLEGLRTGLTQVLHALLAENPARTAQDCLAALA 229

Qy      238  QVFGVESHKTAQVKLCKAYQAEAGKVSFVLRLPLQRAVENNVSRNNVQTRKRV 297
Db      230  QVFGDNEQATIRVKLTAAQQSGERLSAFVLRLEVLQKAMEKALARASADRVRLRQM 289

Qy      298  LSGATLPDKLRDKLMQRKRPGLFALVKLLREEEWEATLG----PDRESLEGLEVA 353
Db      290  LTRAHLTEPLDEALRKLKRMAGRSFLEMIGLVRESEAWASLASRVAQTQEGAGARAG 349

Qy      354  PRPPARI--TGVGAVP-----LPASGNSFDRAPSGQYR 384
Db      350  AQAVARASTKVEAVPGGFRPEPGLLQAGGQAEELLQGLK 391
```

```
RESULT 10
US-10-037-860-4
; Sequence 4, Application US/10037860
; Publication No. US20020123114A1
; GENERAL INFORMATION:
; APPLICANT: Jerome B. Posner
; APPLICANT: Josep O. Dalmau
; APPLICANT: Myrna R. Rosenfeld
; TITLE OF INVENTION: Ma FAMILY POLYPEPTIDES AND ANTI-Ma
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 2581.1004-004
; CURRENT APPLICATION NUMBER: US/10/037,860
; CURRENT FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 09/189,527
; PRIOR FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 329
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-037-860-4

Query Match      31.6%; Score 766.5; DB 13; Length 329;
Best Local Similarity 50.2%; Pred. No. 1.6e-63;
Matches 157; Conservative 50; Mismatches 103; Indels 3; Gaps 2;

Qy      1  MPTLLQDWCRCGEHLNTRRCMLILGIPEDCGDEBFEETLQACRHLGRYRVIQRMFRREE 60
Db      1  MAMTLLDWCRCGMDVNSQRTLLVWGIPIVNCDEAIEETLQAAMPQVS-YRMLGRMFWRREE 59

Qy      61  NQAAILLELAQDIDYALLPREIPKGGPWEVIVKPRNSDGEFNLNRLNRFLEERRTVSDM 120
Db      60  NAKAALILELTGAVDYAAIPREMPGKGWVKVLFKPPSTDAAEFLERLHLFLAREGTVQDV 119

Qy      121  NRVLGSDTNCSPRVTTISPEFTWTAQTLGAAVQPLLEQMLYRELRFVSGNTISIPGALAF 180
Db      120  ARVLGFQNFQPTTPGPEMPAEMLN--ILDNVIQPLVESIWKRLTLFSGKGHPRAWGNF 177

Qy      181  DAMLEHTTEMLQMWQVPEGEKRRRLMECLRGPALQVVSGLRASNASITVBECLAALQOVF 240
Db      178  DPWLEHTNEVLEWQVSDVEKRRRLMESLRGPAADVIRILKSNPNPAITABCLKALEQVF 237

Qy      241  GPVESHKTAQVKLCKAYQAEAGKVSFVLRLPLQRAVENNVSRNNVQTRKRVLSG 300
Db      238  GSVESSRDAQTKFLNTYCNFEKLSAYVIRLEPLLQKVVEKGAIDKDNVNQARLEQVIAG 297

Qy      301  ATLPDKLRDKLKL 313
Db      298  ANHSGAIRRQLWL 310

RESULT 11
US-09-804-014A-40
; Sequence 40, Application US/09804014A
; Publication No. US20030064489A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard
; APPLICANT: Spaderna, Steven
; APPLICANT: Majumder, Kumud
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-721 US
; CURRENT APPLICATION NUMBER: US/09/804,014A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/188,316
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/188,277
; PRIOR FILING DATE: 2000-03-10
```



```
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-014A-73

Query Match      30.6%; Score 740.5; DB 12; Length 312;
Best Local Similarity 48.8%; Pred. No. 4.2e-61;
Matches 148; Conservative 51; Mismatches 101; Indels 3; Gaps 2;

Qy 1 MPTLLQDWCRGHEHLNTRRCMLILGIPEDCGEDEFETLQEAACHLGRYRVIGRMFRREE 60
Db 1 MTLRLLEDWCRGMDMPKALLIAGISQSCSVAIEIEALQAGLAPLGEYLLGRMFRDE 60

Qy 61 NQAAILLELAQDIDYALLPREIPKGGPWEVIVKPRNSDGEFLNRLNRFLEERRTVSDM 120
Db 61 NTKRLLEDWCRGMDMPKALLIAGISQSCSVAIEIEALQAGLAPLGEYLLGRMFRDE 60

Qy 61 NRKVALVGLTAETSHALVPKEIPKGGIWRVIFKPPDPDNTFLSRLNEFLAGEGMTVDEL 120
Db 61 NRKVALVGLTAETSHALVPKEIPKGGIWRVIFKPPDPDNTFLSRLNEFLAGEGMTVDEL 120

Qy 121 NRVLGSDTNCSPRVITISPEFWT--WAOTLGAAVQPLLEOMLYRELRFVSGNTISIPGAL 178
Db 121 SRALGHENGSLDPEQGMIPEMWAPMLAAL--EALQPALQCLKYKLVFSGRESPEEGEE 179

Qy 179 AFDWLHTTEMLOMQVPEGEKRRRLMECLRGPAQVSGLRASNASITVEECIAAQQ 238
Db 180 EFRGWPHHTTQMIKAWQVDPVEKRRRLLESIRGPAQVIRVILKINPLIITVDECLQALEE 239

Qy 239 VFGPVESHKIAQVKLCKAYQEAQKVSFVLRLEPLIQRAVENNVSRNNVNOTRLKRVL 298
Db 240 VFGVTDNPRELQVKYLTYYQKDEKLSAYVLRLEPLQLQVORGAIERDAVNQARLDQVI 299

Qy 299 SGA 301
Db 300 AGA 302

RESULT 14
US-09-804-014A-74
; Sequence 74, Application US/09804014A
; Publication No. US20030064489A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard
; APPLICANT: Spaderna, Steven
; APPLICANT: Majumder, Kumud
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-721 US
; CURRENT APPLICATION NUMBER: US/09/804,014A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/188,316
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/188,277
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/189,139
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: 60/189,140
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: 60/190,401
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/190,231
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 74
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-014A-74

Query Match      30.6%; Score 740.5; DB 12; Length 312;
Best Local Similarity 48.8%; Pred. No. 4.2e-61;
Matches 148; Conservative 51; Mismatches 101; Indels 3; Gaps 2;
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```
Qy 1 MPTLLQDWCRGHEHLNTRRCMLILGIPEDCGEDEFETLQEAACHLGRYRVIGRMFRREE 60
Db 1 MTLRLLEDWCRGMDMPKALLIAGISQSCSVAIEIEALQAGLAPLGEYLLGRMFRDE 60

Qy 61 NQAAILLELAQDIDYALLPREIPKGGPWEVIVKPRNSDGEFLNRLNRFLEERRTVSDM 120
Db 61 NRKVALVGLTAETSHALVPKEIPKGGIWRVIFKPPDPDNTFLSRLNEFLAGEGMTVDEL 120

Qy 121 NRVLGSDTNCSPRVITISPEFWT--WAOTLGAAVQPLLEOMLYRELRFVSGNTISIPGAL 178
Db 121 SRALGHENGSLDPEQGMIPEMWAPMLAAL--EALQPALQCLKYKLVFSGRESPEEGEE 179

Qy 179 AFDWLHTTEMLOMQVPEGEKRRRLMECLRGPAQVSGLRASNASITVEECIAAQQ 238
Db 180 EFRGWPHHTTQMIKAWQVDPVEKRRRLLESIRGPAQVIRVILKINPLIITVDECLQALEE 239

Qy 239 VFGPVESHKIAQVKLCKAYQEAQKVSFVLRLEPLIQRAVENNVSRNNVNOTRLKRVL 298
Db 240 VFGVTDNPRELQVKYLTYYQKDEKLSAYVLRLEPLQLQVORGAIERDAVNQARLDQVI 299

Qy 299 SGA 301
Db 300 AGA 302

RESULT 15
US-10-037-860-11
; Sequence 11, Application US/10037860
; Publication No. US20020123114A1
; GENERAL INFORMATION:
; APPLICANT: Jerome B. Posner
; APPLICANT: Joseph O. Dalmay
; TITLE OF INVENTION: Ma Family Polypeptides and Anti-Ma
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 2581.1004-004
; CURRENT APPLICATION NUMBER: US/10/037,860
; CURRENT FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 09/189,527
; PRIOR FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 283
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-037-860-11

Query Match      25.5%; Score 618.5; DB 13; Length 283;
Best Local Similarity 50.2%; Pred. No. 1.2e-49;
Matches 135; Conservative 44; Mismatches 85; Indels 5; Gaps 3;

Qy 82 IPKGGPWEVIVKPRNSDGEFLNRLNRFLEERRTVSDMNRVLGSDTNCSPRVITISPEF 141
Db 1 VOGKGGVWKVIFKTPNQDTEFLERLNLFLKEGQTVSGMFRALQGEVSGPATVPCISPEL 60

Qy 142 WT--WAOTLGAAVQPLLEOMLYRELRFVSGNTISIPGALAPDAWLEHTTEMLOMQVPEG 199
Db 61 LAHLGQAMAHAPQPLL--PMRYKLRVFGSAVPAPEESFEVWLEQATEIVKEMPVTEA 119

Qy 200 EKRRRLMECLRGPAQVSGLRASNASITVEECIAAQQVGPVESHKIAOVKLCAYQE 259
Db 120 EKKEWLAESLRGPAQVSGLRASNASITVEECIAAQQVGPVESHKIAOVKLCAYQE 179

Qy 260 AGEKVSFVLRLEPLIQRAVENNVSRNNVNOTRLKRVLSGATLPDKLRDKLKLKMRK 319
Db 180 EGEKVSAYVLRLEPLIQRAVENNVSRNNVNOTRLKRVLSGATLPDKLRDKLKLKMRK 239

Qy 320 PPGFIALVKLRBEEWEATLGPDRSLE 348
Db 240 PPSFLMLKVIREEEAEASF--ENESIE 266
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Search completed: September 27, 2004, 17:26:07
Job time : 137.663 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 17:06:36 ; Search time 23.4526 Seconds
(without alignments)
1019.197 Million cell updates/sec

Title: US-10-037-860-13
Perfect score: 2423
Sequence: 1 MPTLLDWCGRGHLNTRRC.....VESGNGWAWDKSHPKSKAK 463

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2394	98.8	462	4	US-09-189-527-13
2	766.5	31.6	329	4	US-09-189-527-4
3	462.5	19.1	195	4	US-09-189-527-7
4	122	5.0	2293	3	US-09-368-530-2
5	110.5	4.6	341	4	US-09-252-991A-20182
6	110	4.5	718	4	US-09-252-991A-32743
7	104	4.3	383	4	US-09-489-039A-11848
8	101.5	4.2	1201	4	US-09-252-991A-32259
9	101	4.2	580	4	US-09-252-991A-22036
10	100	4.1	363	4	US-09-252-991A-26726
11	100	4.1	369	4	US-09-252-991A-22549
12	99.5	4.1	1050	4	US-09-555-554-2
13	99	4.1	639	1	US-08-466-390-2
14	99	4.1	639	1	US-08-470-950-2
15	99	4.1	639	1	US-08-467-781-2
16	99	4.1	639	1	US-08-195-487-2
17	99	4.1	639	2	US-08-483-924-2
18	99	4.1	639	5	PCT-US93-06160-2
19	98.5	4.1	733	4	US-09-489-039A-12568
20	98.5	4.1	820	4	US-09-252-991A-23346
21	97.5	4.0	776	4	US-09-252-991A-28446
22	97.5	4.0	2154	2	US-08-841-349-4
23	97.5	4.0	2154	4	US-09-431-184A-4
24	97	4.0	181	4	US-09-252-991A-26482
25	97	4.0	541	4	US-09-252-991A-30867
26	97	4.0	1958	1	US-07-945-283-2
27	97	4.0	2108	4	US-09-252-991A-31502

RESULT 1
US-09-189-527-13
; Sequence 13, Application US/09189527A
; Patent No. 6387639
; GENERAL INFORMATION:
; APPLICANT: Jerome B. Posner
; APPLICANT: Josep O. Dalmau
; APPLICANT: Myrna R. Rosenfeld
; TITLE OF INVENTION: Ma Family Polypeptides and Anti-Ma
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: SLK98-01
; CURRENT APPLICATION NUMBER: US/09/189,527A
; CURRENT FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 462
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-189-527-13

ALIGNMENTS

Query Match	98.8%	Score	2394	DB	4	Length	462
Best Local Similarity	100.0%	Pred. No.	3e-247				
Matches	457	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	7	QDWCGRGHLNTRRCMLILGIPEDCGEDFETLQACRHLGRYVIGRMFRRENAQAIL	66				
Db	1	QDWCGRGHLNTRRCMLILGIPEDCGEDFETLQACRHLGRYVIGRMFRRENAQAIL	60				
Qy	67	LELAQDIDYALLPREIPKGGPMEVIVKPRNSDGEFLNRLNRFLEEBRRTVSDMNRVLGS	126				
Db	61	LELAQDIDYALLPREIPKGGPMEVIVKPRNSDGEFLNRLNRFLEEBRRTVSDMNRVLGS	120				
Qy	127	DTNCSAPRVITSPBFTWAOITLGAAVQPLLEQMLYRELRFVPSGNTISIPGALAFDAMLEH	186				
Db	121	DTNCSAPRVITSPBFTWAOITLGAAVQPLLEQMLYRELRFVPSGNTISIPGALAFDAMLEH	180				
Qy	187	TTEMLOWQVPEGEKRRRLMECLRGPAQVVGSLRASNASITVEECALAOQVFGPVESH	246				
Db	181	TTEMLOWQVPEGEKRRRLMECLRGPAQVVGSLRASNASITVEECALAOQVFGPVESH	240				
Qy	247	KIAQVKLCKAYQAGEKVSFVLRLPQLQRAVNNVSRNNVQTRKRLKVLGATLPDK	306				
Db	241	KIAQVKLCKAYQAGEKVSFVLRLPQLQRAVNNVSRNNVQTRKRLKVLGATLPDK	300				
Qy	307	LRDKLKLKMKQRKPPGFLALVKLLREEEWEATLGPDRSLEGLVAPRPPARITGVAV	366				
Db	301	LRDKLKLKMKQRKPPGFLALVKLLREEEWEATLGPDRSLEGLVAPRPPARITGVAV	360				
Qy	367	PLFASGNSFARPSQGYRRRRGRGQHRGGVARGSGRKRKRKHTFCYSCGEDCHTRVQ	426				

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Db 361 PIPASGNSFDAPSQYRRRGQHRGQVAPAGSGRKRKHRTFCISGEGDHIRVQ 420
QY 427 CINPSNLLVKKQKAAVESGNGNWNWDKSHPKSKAK 463
Db 421 CINPSNLLVKKQKAAVESGNGNWNWDKSHPKSKAK 457
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RESULT 2

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US-09-189-527-4
; Sequence 4, Application US/09189527A
; Patent No. 6387639
; GENERAL INFORMATION:
; APPLICANT: Jerome B. Posner
; APPLICANT: Josep O. Dalmau
; APPLICANT: Myrna R. Rosenfeld
; TITLE OF INVENTION: Ma Family Polypeptides and Anti-Ma
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: SLK98-01
; CURRENT APPLICATION NUMBER: US/09/189,527A
; CURRENT FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 329
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-189-527-4
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Query Match 31.6%; Score 766.5; DB 4; Length 329;
Best Local Similarity 50.2%; Pred. No. 2.9e-73;
Matches 157; Conservative 50; Mismatches 103; Indels 3; Gaps 2;

QY 1 MPTLLQDWCRCGHLNTRCMLILGIPEDCGEDEFETLQACRHLGRYRVIGMFRREE 60
Db 1 MAMTLLDWCRCGMDVNSQRTLLVWGPVNCDEAIEETLQAAMPQVS-YRMLGRMFWREE 59

QY 61 NQAAILLEAQDIDYALLPREIPKGGPWVIVKPRNSDGEFLNRLNRLLEERTVSDM 120
Db 60 NAKAALLEITGAVDYAAIAPREMPKGGVWVKVLPKPTSDAEFLRLHLFLAREGWVQDV 119

QY 121 NRVLGSDTNCSPRVTTISPEFTWTAOTLGAAPVLPLEQMLYRELVRVFSGNTISIPGALAF 180
Db 120 ARVLGQNPQTPPGPMPAEMLNYY--ILDNVIQPLVESIWKELTIFSGKHGHPRAWGNF 177

QY 181 DAWLEHTTEMLOWQVPEGEKRRRLMECLRGPALQVWSGLRASNASITVEECLAAALQQVF 240
Db 178 DPWLEHTNEVLBEWQVSDVEKRRRLMESLRGPAADVIRILKSNNPATITTAECLEQVVF 237

QY 241 GPVESHKIAQVKLCKAYQAGEKGVSSFVLRLLEPLLQRAVENNVSRNNVQTRKRVLSG 300
Db 238 GSVESRDAQIKFLNTYQNGEKLISAYVIRLEPLLQKRVVEKGAIDKONVNOARLEQVIAG 297

QY 301 ATLPDKLRDKLKL 313
Db 298 ANHSGAIRQLWL 310
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RESULT 3

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US-09-189-527-7
; Sequence 7, Application US/09189527A
; Patent No. 6387639
; GENERAL INFORMATION:
; APPLICANT: Jerome B. Posner
; APPLICANT: Josep O. Dalmau
; APPLICANT: Myrna R. Rosenfeld
; TITLE OF INVENTION: Ma Family Polypeptides and Anti-Ma
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: SLK98-01
; CURRENT APPLICATION NUMBER: US/09/189,527A
; CURRENT FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 7
; LENGTH: 195
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-189-527-7

Query Match 19.1%; Score 462.5; DB 4; Length 195;
Best Local Similarity 47.7%; Pred. No. 4.2e-41;
Matches 93; Conservative 34; Mismatches 65; Indels 3; Gaps 2;

QY 2 PTLTLLQDWCRCGHLNTRCMLILGIPEDCGEDEFETLQACRHLGRYRVIGMFRREEN 61
Db 1 PLALLDWCRCIMSDVQKSLMVTGIPADPEEAIEQVLTLLKSLGRYLLGKIFRKQEN 60

QY 62 AQAAILLEAQDIDYALLPREIPKGGPWVIVKPRNSDGEFLNRLNRLLEERTVSDMN 121
Db 61 ANAVILLELEDDTDSVAIPSEVQKGGVWVKVFPKPNQDTEFLERLNLFLKEKGQTVSGMF 120

QY 122 RVLGSDTNCSPRVTTISPEFTW--WAOTLGAAPVLPLEQMLYRELVRVFSGNTISIPGALA 179
Db 121 RALGQEAALSPATVPCISPELLAHLGQAMAHAPQPLL-PMRYKLVFVSGSAVPAPEEES 179

QY 180 FDWLEHTTEMLOWM 194
Db 180 FEVWLEQATEIVKEM 194
```

RESULT 4

```
US-09-368-590-2
; Sequence 2, Application US/09368590
; Patent No. 6187563
; GENERAL INFORMATION:
; APPLICANT: Solimena, Michele
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
; TITLE OF INVENTION: AUTOANTIGENS OF AUTOIMMUNE DISEASES
; FILE REFERENCE: 101918-200 (OCR-941)
; CURRENT APPLICATION NUMBER: US/09/368,590
; CURRENT FILING DATE: 1999-08-04
; EARLIER APPLICATION NUMBER: 60/095,657
; EARLIER FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2293
; TYPE: PRT
; ORGANISM: Human
US-09-368-590-2
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Query Match 5.0%; Score 122; DB 3; Length 2293;
Best Local Similarity 25.1%; Pred. No. 0.0069;
Matches 100; Conservative 57; Mismatches 144; Indels 98; Gaps 24;

QY 60 ENAQAILLLEAQDIDYALLPREIPGK-----GGFWEVIVKPRNSDGEFL---NR 105
Db 733 EPRQAALLEEA-----ALLAERFPAQAAXLHQGAEBLGAEWGALASAAACGSAVAAAGR 787

QY 106 LNRFLEERTVSDMNRVLGSDTNCSPRVTTISPEFTWTAOTLGAAPVLPLEQMLYRE-- 163
Db 788 LQRFLLDLDLAFLOWVRAQEAAGSGSGP----LPNSLEEDALLAHAAALKEEVDQREED 843

QY 164 -LRVFSGN--TISPGA-----LAFDAWLEHTT-----EMLQWQVPEGEKRRRLMEC--- 208
Db 844 YARIVAASEALLAADGAELGPGGLALDEWLPHELGWHKLLGLWKA---RRKALVQAHIY 899

QY 209 ---LRG--PALQVVSQ--LRASNASI--TVEECLAAALQQVFGPVESHKIAQVKLCKAYQE 259
Db 900 QULFRLDRLQALVVLNRQENALSGAELPGTVESVEEALKQHRDPLTTMELSSQQQKQAVQA 959

QY 260 A-----GKVVSSFVLRLEPLQLQRAVENNVSRNV---NOTRLKRVLS-----G 300
Db 960 AEGLLRQGNITYGEQAQEAQVTR---LLEKQENQLRAQQWQKQLHDQLEQLHFLRDCHELD 1016

QY 301 ATLPDKL-----RDKLKLKQRRKPPGFALVKLLREERWEATL-----GPDRESLE-- 348
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32743

Query Match      4.5%; Score 110; DB 4; Length 718;
Best Local Similarity 21.7%; Pred. No. 0.02;
Matches 70; Conservative 31; Mismatches 93; Indels 128; Gaps 16;

Qy 242 PVESHKIAQVKLCKAYQAEKGVSVLRLEPL-----LQRAVE----- 280
Db 122 PEKPHVVERPRHVDAYRQPGQATR---RLSPFGPRRRRTDRHAGGGPQRALHLARA 178
Qy 281 -----NNVGSRRNVNQTRLKRVLSGATLPDKLRLKMKQRRKPPG---FLALV 327
Db 179 DGHRRCLHPLPAGRRGLPRRLRGAV--ANLPSRADH---GVRRRPAGGGLFRGLA 232
Qy 328 KLLREBEWEATLGPDRSLEGLVAPRPPAR-ITG-----VGAVPLPASGNSF 375
Db 233 QRTVPGDAARTPAADRRDRRLRRRAPARGTGRGGGQRPRLPAGAIQPA----- 287
Qy 376 DARPSQGYRRRG-----RQHR----- 393
Db 288 -GEPPQGLQRRPCPPAFPPRSAGGARGHLRHRPAPVRRRARPGRSQKRVAAG 346
Qy 394 RGVVARAGSRK-----RKHTFCVSCGEDGHIRVQCINPSNLLL-----VKQK 439
Db 347 RGGPRAGLPAHRRRHGFLPRRHSYRPA---DGH-RAGLPGPRSYLOGAPGDPVHR 402
Qy 440 KQAAVESGNGNMAWDKSHPKSK 461
Db 403 AHQAPAGRG-----HPRPR 417

RESULT 7
US-09-489-039A-11848
; Sequence 11848, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11848
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11848

Query Match      4.3%; Score 104; DB 4; Length 383;
Best Local Similarity 22.5%; Pred. No. 0.03;
Matches 60; Conservative 44; Mismatches 91; Indels 72; Gaps 12;

Qy 114 RRTVSDMNRVLGSDTNCSPRVTTISPEFTWQTLGAQVQPLLEQMLYRELURVFSGNTIS 173
Db 118 QRGAAELHR-CRSETLCTLRATISSSFITHPRNNNDIAHNLAQ---VRD-----K 164
Qy 174 IPGALADAWLEHTTEMLQMWQVPEGKRRRLMECLRGPALQVVSGLRASNASITVEECL 233
Db 165 ISGAAA-----RCGRAPEVTVLLAVSKTKPASAIEEAI 197
Qy 234 AALQOVFGPVESHKIAQVKLCKAYQAEKGVSVLRLEPLQRA-----VENNVVSRNV 289
Db 198 AAGQRAFQ--ENV-----VQGVKINH-----QAGVSGLOWHFIGPLQS 237
Qy 290 NQTRL-KRVLSGATLPDKLRLKMKQRRKPPGFLALVKLLRE--BEWEATLGPDRS 346
Db 238 NKSRLVAEHFDWCHTVDRLKTIATRLNEQR---PAHLPLKVLQIINISDEQSKSGIPLEA 294
; LENGTH: 718
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20182
; Sequence 20182, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20182
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20182

Query Match      4.6%; Score 110.5; DB 4; Length 341;
Best Local Similarity 24.3%; Pred. No. 0.005; DB 4; Length 341;
Matches 66; Conservative 22; Mismatches 109; Indels 75; Gaps 11;

Qy 208 CLRGPALQVSGLRASNASITVEECLAALQOVFGPVESHKIAQVKLCKA----- 256
Db 16 CLGCP-----VDGHPAKHASLRGNGKLRHGVPAQH--RLCFAGGQGPDPAPAH 67
Qy 257 -----YQEA-----GEKVSVFVLRLEPLLRQAVENNVVSRNVNQTRLKRVLSGATLPDK 306
Db 68 PPAQPHYSSHPRHGRPALPALRADPLRLRGRGR--SRRPCPTRRQ---AEAADFDR 122
Qy 307 LRDLKLMKQRRKPPGFLALVKLREBEWEATLGPDRSLE----- 348
Db 123 HRPALDRPHRLRP--AVPRDLRPHGQPRAGPARGLRRHGRGLRAARFELHPPA 179
Qy 349 -----GLEVAPRPPARITGVGAVPLPASGNSFDRPQSGYRR--RRGRGQHR 394
Db 180 HRRDLQHSRLAGVPAPERHAERAFAGAGQPRLPAPGQPGGAAGSLAVERSQRPGNGLHR 239
Qy 395 -----GGVARAGSRGRKRTITFCVSCGEDGH 422
Db 240 LAVPGQCRRRDRGNPLRTGHR--HPAGVFGH 269

RESULT 6
US-09-252-991A-32743
; Sequence 32743, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32743
; LENGTH: 718
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```

; LENGTH: 1050
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-555-554-2

Query Match      4.1%; Score 99.5; DB 4; Length 1050;
Best Local Similarity 20.1%; Pred. No. 0.49;
Matches 72; Conservative 51; Mismatches 124; Indels 111; Gaps 17;

Qy 35 FEETLOEACRHLGRYVIGRMFRRENAQAILLELAQIDYALLPREIP----- 83
Db 175 FQGIQKQKAPLERLQSHRQFQARVSRQT--LLALEKEEEEEVEFSSVQPSRTLAELKSK 233
Qy 84 GK-----GGPWEVIYKPNSDGEFLNRLNRFLEEBERTVSDMNRVLGSDTNCSP 133
Db 234 GKKTARAPIIRVVGALKAPSNRGLQNPFPQOMQ---NNSRITVFDENADEASTAELSKP 290
Qy 134 RVTISPEFTWAQTLGAAVOPLLBOMLYRELRFVSGMT-----ISIPGAL 178
Db 291 --TVQP-----W-----IAPPMPRAKENELQAGPWNIGRSLHRPRGNTASLIAVPAVL 337
Qy 179 -AFDAWLEHTTEM-----LQMWQVPEGEKRRRLM 206
Db 338 PSFTPYVEETAQOPVMTCKIEPSINHILSTRKPKKEGDPLORVQSHQQAEBKKKKMM 397
Qy 207 ECLRGPALQVVGSLRASNASITVEECLAAQOQVFPVESHKIAQVKLKAYQAEAGEKVS 266
Db 398 YCKE---KIYAGV---GEFSFEIRA---EVFR-----KKLKEQREA-ELLTS 435
Qy 267 FVLRLPLELQRAVENNVVSRNVNQTRLKRV--LSGATLPDKLRDKLKMQRKPPG 322
Db 436 AKRAE--MQQIEEMKKLKEIQTTOBERTGDOQOEBTMTKTKLQIASESKIPG 491

RESULT 13
US-08-466-390-2
; Sequence 2, Application US/08466390
; Patent No. 5686562
; GENERAL INFORMATION:
; APPLICANT: TOURKATLY, GARY
; TITLE OF INVENTION: LIDGARD, GRAHAM P
; TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
; TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,390
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: MTP-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 639 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```

```

; LENGTH: 1050
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-555-554-2

Query Match      4.1%; Score 100; DB 4; Length 369;
Best Local Similarity 21.1%; Pred. No. 0.077;
Matches 63; Conservative 31; Mismatches 108; Indels 96; Gaps 12;

Qy 168 SGNITISIPGALAFDAWLEHTTTEMLQMMQVPEGEKRRRLMECLRGPALQVVGSLRASNASI 227
Db 106 AGGTVDPGG-----LRRRAQRIIVHRAAPRAFRPEYFHC--GHSQFLLCSMRQNSK- 156
Qy 228 TVECLAAQVQFVGVESHKIAQVKLKAYQAEAGEKVSFVLRLEPLIORA--VENNVVS 285
Db 157 -----TEPFHVLV-----VPGEPYAS-----PALPAAGPVPGPVVD 188
Qy 286 RNVNQ-----TLKRVLSGATLPDKLRDKLKMQRKRP 320
Db 189 RRRRCRTVLPAGGLRALRGRAQCTGCLVRRGRRAFPAGASREDQRRERAGAAARRRA- 247
Qy 321 PGFLALVKLLEEEBEWEATLPGDRESLEGLVAPRPPARITGVGAVPLPASGNSFDARPS 380
Db 248 --AASHRRQRERQLGARQRPQRH-----PSHRRRAPGQRTFFPATGQGRAGRAR-L 295
Qy 381 QGYRRRRRGQHR-----GGVARAGSRGRKRRKHTFCYSCGEDGHIR 424
Db 296 RGIRRRRAPLVHRQFLRPSRPSQAPGGGLALAPGQGGERHLRHP-----GRRGLVR 348

RESULT 12
US-09-555-554-2
; Sequence 2, Application US/09555554
; Patent No. 6593098
; GENERAL INFORMATION:
; APPLICANT: Yen, Timothy J.
; APPLICANT: Chan, Gordon
; APPLICANT: Jablonski, Sandra
; TITLE OF INVENTION: No. 6593098el Genes Encoding Proteins Involved
; TITLE OF INVENTION: in Mitotic Checkpoint Control and Methods of Use Thereof
; FILE REFERENCE: FCCC 97-12
; CURRENT APPLICATION NUMBER: US/09/555,554
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/US98/25415
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2

```

US-08-466-390-2

```
Query Match 4.1%; Score 99; DB 1; Length 639;
Best Local Similarity 20.8%; Pred. No. 0.24;
Matches 79; Conservative 57; Mismatches 162; Indels 82; Gaps 17;

QY 68 ELAQDIDYALLPREIPGKGPWEVIVKPRNSDGEFLNRLNRFLEEBERRTVSDMNRVLGSD 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 250 DFKRELD-SITPEVLPG-----WKGMSVSLADKLSTDDLSLIAHAHRRIDQLNRELAQ 304

QY 128 TNCASPRVTISPEFTWAQ--TLGAAVQPLLE-----QMLYRELRFVSGNTISIP 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 305 KATEKHITLAEKQKLEEKRAFDASAVAKALEHHRSEIOAEQDRKTEEVVDAMENEMRTP 364

QY 176 GALAFDAWLEHITEMLQMWQVPEGR-----RLMECLRGPALOV--VSGLRASASITV 229
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 365 SPTA-----AAHTDHLRDVLRVQEQELKSEFQNLSEQLQFRRLSQEQVDNFTLDI 420

QY 230 EECLAAQOVFGVESHKIAQVKLCKAYQ-----EAGEKVSSFVLRLEPLLQRAVEN 281
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 421 NTAYARLRGIEQAVQSHAVEAEERAKAQWLVSVEALKYSMTKSSAETPTIP-LGSAVE- 478

QY 282 NVVSRNVNQTRLKRVLSGATLPDKLRDKL---KLMKQRKPPGFLALVKLLEEEWEA 338
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 479 --AIKANCSDNEFTQALTAIIPESLTRGVYSEETLRAR-----FYAVQKLARR-----VA 527

QY 339 TLGPDRES-----LEGLEVP-----RPPARITGVGAVPLPASGNSFDARPSQCYRRR 386
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 528 MIDETRNSLYQVFLSYQLSLLLFPPOQLKPPPEL-----CPEDINTFKLLSYASYCIE 580

QY 387 RG-----RGQHR 394
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 581 HGDLELAAKFVNQKGESRR 600
```

RESULT 14

```
US-08-470-950-2
; Sequence 2, Application US/08470950
; Patent No. 5698439
; GENERAL INFORMATION:
; APPLICANT: TOKUATLY, GARY
; APPLICANT: LIDGARD, GRAHAM P
; TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
; TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,950
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: MTP-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 639 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
```

; MOLECULE TYPE: protein

US-08-470-950-2

```
Query Match 4.1%; Score 99; DB 1; Length 639;
Best Local Similarity 20.8%; Pred. No. 0.24;
Matches 79; Conservative 57; Mismatches 162; Indels 82; Gaps 17;

QY 68 ELAQDIDYALLPREIPGKGPWEVIVKPRNSDGEFLNRLNRFLEEBERRTVSDMNRVLGSD 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 250 DFKRELD-SITPEVLPG-----WKGMSVSLADKLSTDDLSLIAHAHRRIDQLNRELAQ 304

QY 128 TNCASPRVTISPEFTWAQ--TLGAAVQPLLE-----QMLYRELRFVSGNTISIP 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 305 KATEKHITLAEKQKLEEKRAFDASAVAKALEHHRSEIOAEQDRKTEEVVDAMENEMRTP 364

QY 176 GALAFDAWLEHITEMLQMWQVPEGR-----RLMECLRGPALOV--VSGLRASASITV 229
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 365 SPTA-----AAHTDHLRDVLRVQEQELKSEFQNLSEQLQFRRLSQEQVDNFTLDI 420

QY 230 EECLAAQOVFGVESHKIAQVKLCKAYQ-----EAGEKVSSFVLRLEPLLQRAVEN 281
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 421 NTAYARLRGIEQAVQSHAVEAEERAKAQWLVSVEALKYSMTKSSAETPTIP-LGSAVE- 478

QY 282 NVVSRNVNQTRLKRVLSGATLPDKLRDKL---KLMKQRKPPGFLALVKLLEEEWEA 338
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 479 --AIKANCSDNEFTQALTAIIPESLTRGVYSEETLRAR-----FYAVQKLARR-----VA 527

QY 339 TLGPDRES-----LEGLEVP-----RPPARITGVGAVPLPASGNSFDARPSQCYRRR 386
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 528 MIDETRNSLYQVFLSYQLSLLLFPPOQLKPPPEL-----CPEDINTFKLLSYASYCIE 580

QY 387 RG-----RGQHR 394
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 581 HGDLELAAKFVNQKGESRR 600
```

RESULT 15

```
US-08-467-781-2
; Sequence 2, Application US/08467781
; Patent No. 5780596
; GENERAL INFORMATION:
; APPLICANT: TOKUATLY, GARY
; APPLICANT: LIDGARD, GRAHAM P
; TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
; TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,781
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: MTP-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 639 amino acids
; TYPE: amino acid
```



```
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-781-2

Query Match      4.1%; Score 99; DB 1; Length 639;
Best Local Similarity 20.8%; Pred. No. 0.24;
Matches 79; Conservative 57; Mismatches 162; Indels 82; Gaps 17;

Qy 68 ELAQDIDYALLPREIPGKGPGWEVIVKPRNSDGEFLNRLNRFLEEEERTVSDMNRVLGSD 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 250 DFKRELD-SITPEVLPG-----WKGMSVSDLADKLDLSTDDLSLJAHARRIDQLNRELAQ 304
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 128 TNCAPRVITISPEFTWAQ--TLGAAVQPLLE-----QMLYRELRFVSGNTISIP 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 305 KATEKQHITLALQKLEEKRAFDSDAVAKALEHHRSEIQAEQDRKIEEVRDAMENEMRTP 364
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 176 GALAFDAWLEHTTETMLQMWQVPEGEKR---RRIMECLRGFPALQV--VSGLRASNASITV 229
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 365 SPTA-----AAHTDHLRDVLVQEQELKSEFEQNLSEKLSQELOFRRLSQEQVDNFTLDI 420
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 230 EECALAQVFGPVESHKIAQVKLCKAYQ-----EAGEKVSSFVLRLEPLQRAVEN 281
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 421 NTAYARLRGIEQAVQSHAVAEAEARKAHQLWLSVEALKYSMTSSAETPTIP-LGSAVE- 478
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 282 NVYSRRNVNQLKRVLSGATLPDKLKDCL---KLMQQRKPPGFLALVKLLREEEWEA 338
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 479 --AIKANCSDNEFTQALTAIIPPESTLGRVYSEETLRAR-----FYAVQKLARR-----VA 527
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 339 TLGPDRES-----LEGLEVAP---RPPARITGVGAVPLPASGNSFDARPSQGYRRR 386
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 528 MIDETRNSLYQYFLSYLSYLSQSLLLFPFPQQLKPPPEL-----CPEDINTFKLLSYASYCIE 580
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 387 RG-----RGQHR 394
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 581 HGDLELAAKFVNQLKGESRR 600
```

Search completed: September 27, 2004, 17:11:20
Job time : 25.4526 secs

Blank

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 27, 2004, 17:02:20 ; Search time 77.9232 Seconds
(without alignments)
1678.826 Million cell updates/sec

Title: US-10-037-860-13

Perfect score: 2423

Sequence: 1 MPLTLQDWCRGEHLNTRRC.....VESGNGWAWDKSHPKSKAK 463

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2423	100.0	463	3 AAB12529	Human Ma5
2	2423	100.0	463	3 AAB42315	Human ORF
3	2283.5	94.2	455	5 ABB05727	Human sig
4	893.5	36.5	452	6 AAO16179	Human pro
5	836.5	34.5	364	7 ADC08977	Onconeuro
6	818	33.8	353	3 AAB74701	Human mem
7	768.5	31.7	351	4 AAE01340	Human gen
8	768.5	31.7	351	4 AAB74695	Human mem
9	768.5	31.7	351	4 AAU08664	Human NOV
10	768.5	31.7	399	6 ADA54410	Human pro
11	768.5	31.7	399	6 ABG99947	Human nov
12	755.5	31.2	329	3 AAB12525	Human ORF
13	740.5	30.6	312	3 AAB43023	Human ORF
14	617.5	25.5	283	3 AAB12528	Human Ma4
15	476.5	19.7	280	4 AAE01336	Human gen
16	462.5	19.1	195	3 AAB12526	Human Ma2
17	454.5	18.8	237	4 AAB94854	Human pro
18	429.5	17.7	403	5 AAM51624	KIAA0883-
19	423.5	17.5	403	5 ABB97495	Human NOV
20	423.5	17.5	403	6 ABO14772	Novel hum
21	421.5	17.4	403	6 ABO14773	Novel hum
22	415.5	17.1	402	4 AAB60478	Human cel
23	384.5	15.9	337	4 AAM25693	Human pro
24	359	14.8	80	4 ABB15036	Human ner
25	351.5	14.5	439	6 ABP75736	Human sec

ALIGNMENTS

RESULT 1

AAB12529

ID AAB12529 standard; protein; 463 AA.

XX AC AAB12529;

XX DT 02-NOV-2000 (first entry)

XX DE Human Ma5 protein SEQ ID NO:13.

XX KM Ma1; Ma2; Ma3; Ma4; Ma5; paraneoplastic limbic encephalitis; diagnosis;

KW paraneoplastic syndrome; neoplasm; colon cancer; brainstem encephalitis;

KW breast cancer; parotid gland cancer; lung cancer; testicular cancer;

KW germ-cell tumour.

XX OS Homo sapiens.

XX PN JP2000146982-A.

XX PD 26-MAY-2000.

XX PF 10-NOV-1999; 99JP-00320171.

XX PR 10-NOV-1998; 98US-00189527.

XX PA (SLOK) SLOAN KETTERING INST CANCER RES.

XX WPI; 2000-468119/41.

XX N-PSDB; AAA60837.

PT Diagnosing paraneoplastic syndrome e.g. paraneoplastic limbic

PT encephalitis or neoplasm e.g. colon cancer comprising assessing a test

PT sample for the presence or absence of antibodies to a Ma family

PT polypeptide.

XX Claim 48; Fig 9-10; 27pp; Japanese.

CC The present invention describes a method for diagnosing a paraneoplastic syndrome or neoplasm. The method comprises assessing a test sample for the presence or absence of antibodies to a Ma family polypeptide (I). The method is used to diagnose a paraneoplastic syndrome especially paraneoplastic limbic encephalitis and/or brainstem encephalitis or neoplasm in an individual. The method diagnoses the neoplasm by assessing antibodies to (i) preferably Ma1, which is indicative presence of breast cancer, colon cancer, parotid gland cancer, lung cancer, testicular cancer, and germ-cell tumours or Ma2, which is indicative of testicular cancer, germ-cell tumour, and lung cancer. The present sequence is the Ma5 protein as given in the present invention

```
XX SQ Sequence 463 AA;
Query Match 100.0%; Score 2423; DB 3; Length 463;
Best Local Similarity 100.0%; Pred. No. 5.6e-231;
Matches 463; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPTLLQDWCRCGEHLNTRCMLILGIPEDCGEDEFETLQACRHLGRYRVIGRMFRREE 60
DB 1 MPTLLQDWCRCGEHLNTRCMLILGIPEDCGEDEFETLQACRHLGRYRVIGRMFRREE 60
QY 61 NQAAILLELAQDIDYALLPREIPGKGPWEIVKPRNSDGEFLNRLNRFLEBERRTVSDM 120
DB 61 NQAAILLELAQDIDYALLPREIPGKGPWEIVKPRNSDGEFLNRLNRFLEBERRTVSDM 120
QY 121 NRVLGSDTNCSPRVVTISPEFTWTAQTGAAVQPLLEQMLYRELRFVSGNTTISIPGALAF 180
DB 121 NRVLGSDTNCSPRVVTISPEFTWTAQTGAAVQPLLEQMLYRELRFVSGNTTISIPGALAF 180
QY 181 DAWLEHTTTEMLQWQVPEGEKRRRLMECLRGPAQVVSGLRASNASITVEECALAAQQVF 240
DB 181 DAWLEHTTTEMLQWQVPEGEKRRRLMECLRGPAQVVSGLRASNASITVEECALAAQQVF 240
QY 241 GPVESHKIAQVKLCAYQAGEKVSFVLRLPELQORAVENNVSRRNVNQTRLKRVLSG 300
DB 241 GPVESHKIAQVKLCAYQAGEKVSFVLRLPELQORAVENNVSRRNVNQTRLKRVLSG 300
QY 301 ATLPDKLRDKLKLKMKQRRKPPGFLALVKLLREEEWEATLGPDRSLEGLVAPRPARI 360
DB 301 ATLPDKLRDKLKLKMKQRRKPPGFLALVKLLREEEWEATLGPDRSLEGLVAPRPARI 360
QY 361 TGVGAVPLPASGNSFDARPSQGYRRRGRGQHRGGVAGRSGSRKRKHTFCYSCGD 420
DB 361 TGVGAVPLPASGNSFDARPSQGYRRRGRGQHRGGVAGRSGSRKRKHTFCYSCGD 420
QY 421 GHIRVQCINPSNLLLVKQKQAAVESGNGNWADKSHPKSKAK 463
DB 421 GHIRVQCINPSNLLLVKQKQAAVESGNGNWADKSHPKSKAK 463
RESULT 2
AAB42315
ID AAB42315 standard; protein; 463 AA.
AC AAB42315;
XX
XX 08-FEB-2001 (first entry)
XX
XX Human ORFX ORF2079 polypeptide sequence SEQ ID NO:4158.
XX
XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
XX vunerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
XX immunostimulant; osteopathic; antiarthritic; immunosuppressant; cardiant;
XX hypotensive; dermatological; immunosuppressive; antiinflammatory;
XX antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
XX antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
XX neurodegenerative disorder; osteoarthritis; graft vs host disease;
XX cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
XX cholesterol ester storage; systemic lupus erythematosus; infection;
XX severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
XX allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
XX bone damage; cartilage damage; antiinflammatory disease; coagulation;
XX thrombosis; contraceptive.
XX
XX Homo sapiens.
XX
XX WO200058473-A2.
XX
XX 05-OCT-2000.
XX
XX 31-MAR-2000; 2000WO-US008621.
XX
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PR 31-MAR-1999; 99US-0127607P.
PR 02-APR-1999; 99US-0127636P.
PR 05-APR-1999; 99US-0127728P.
PR 30-MAR-2000; 2000US-00540763.
XX (CURA-) CURAGEN CORP.
XX
XX Shinkets RA, Leach M;
XX
XX WPI; 2000-602362/57.
XX N-PSDB; AAC76524.
XX
XX Novel nucleic acids and peptides derived from open reading frame X,
XX useful for treating e.g cancers, proliferative disorders,
XX neurodegenerative disorders and cardiovascular disease.
XX
XX Claim 11; Page 3345-3347; 5507pp; English.
XX
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
XX which represent the human ORFX open reading frames 1 to 3161. The ORFX
XX sequences have activities such as: cytostatic; hepatotropic; vunerary;
XX antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
XX anticovulsant; antiarthritic; immunosuppressant; immunostimulant;
XX cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
XX dermatological; immunosuppressive; antiinflammatory; antibacterial;
XX antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
XX sequences can be used for determining the presence of or predisposition
XX to, or preventing or treating pathological conditions associated with an
XX ORFX-associated disorder. The nucleic acids can be used to express ORFX
XX proteins in gene therapy vectors. The proteins and nucleic acids may be
XX used to treat cancers, proliferative disorders, neurodegenerative
XX disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
XX diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
XX storage, systemic lupus erythematosus, severe combined immunodeficiency
XX (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
XX disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
XX cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
XX enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX
XX Sequence 463 AA;
```

```
Query Match 100.0%; Score 2423; DB 3; Length 463;
Best Local Similarity 100.0%; Pred. No. 5.6e-231;
Matches 463; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPTLLQDWCRCGEHLNTRCMLILGIPEDCGEDEFETLQACRHLGRYRVIGRMFRREE 60
DB 1 MPTLLQDWCRCGEHLNTRCMLILGIPEDCGEDEFETLQACRHLGRYRVIGRMFRREE 60
QY 61 NQAAILLELAQDIDYALLPREIPGKGPWEIVKPRNSDGEFLNRLNRFLEBERRTVSDM 120
DB 61 NQAAILLELAQDIDYALLPREIPGKGPWEIVKPRNSDGEFLNRLNRFLEBERRTVSDM 120
QY 121 NRVLGSDTNCSPRVVTISPEFTWTAQTGAAVQPLLEQMLYRELRFVSGNTTISIPGALAF 180
DB 121 NRVLGSDTNCSPRVVTISPEFTWTAQTGAAVQPLLEQMLYRELRFVSGNTTISIPGALAF 180
QY 181 DAWLEHTTTEMLQWQVPEGEKRRRLMECLRGPAQVVSGLRASNASITVEECALAAQQVF 240
DB 181 DAWLEHTTTEMLQWQVPEGEKRRRLMECLRGPAQVVSGLRASNASITVEECALAAQQVF 240
QY 241 GPVESHKIAQVKLCAYQAGEKVSFVLRLPELQORAVENNVSRRNVNQTRLKRVLSG 300
DB 241 GPVESHKIAQVKLCAYQAGEKVSFVLRLPELQORAVENNVSRRNVNQTRLKRVLSG 300
QY 301 ATLPDKLRDKLKLKMKQRRKPPGFLALVKLLREEEWEATLGPDRSLEGLVAPRPARI 360
DB 301 ATLPDKLRDKLKLKMKQRRKPPGFLALVKLLREEEWEATLGPDRSLEGLVAPRPARI 360
QY 361 TGVGAVPLPASGNSFDARPSQGYRRRGRGQHRGGVAGRSGSRKRKHTFCYSCGD 420
DB 361 TGVGAVPLPASGNSFDARPSQGYRRRGRGQHRGGVAGRSGSRKRKHTFCYSCGD 420
```

QY 421 GHIRVQCINPSNLLLVKQKQAAVESGNGNNAWDKSHPKSKAK 463
 DB 421 GHIRVQCINPSNLLLVKQKQAAVESGNGNNAWDKSHPKSKAK 463

RESULT 3

ABB05727
 ID ABB05727 standard; protein; 455 AA.

XX ABB05727;
 AC ABB05727;
 DT 30-APR-2002 (first entry)

XX Human signal transduction protein clone tes3_5k22.

XX Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
 KW gene therapy.

XX Homo sapiens.

XX WO2001198454-A2.

XX 27-DEC-2001.

XX 25-APR-2001; 2001WO-IB002050.

XX 25-APR-2000; 2000US-0199380P.

XX (GEHU-) GERMAN HUMAN GENOME PROJECT.

XX Wiemann S;

XX WPI; 2002-055860/07.

XX N-PSDB; ABA93764.

XX Human cDNA sequences and clones derived from human fetal brain, fetal
 PT kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
 PT screening and therapy.

XX Claim 1; Page 382; 61pp; English.

XX The present invention describes assemblages and computer readable media
 CC comprising novel human cDNA sequences and clones derived from human
 CC foetal brain, foetal kidney, melanoma, testis and amygdala cDNA
 CC libraries. ABA93702 to ABA93766 represent human cDNA sequences from the
 CC present invention which encode the proteins given in AB805662 to
 CC AB805729. The human cDNA sequences and clones can be used in gene
 CC therapy. The clones may be used in a variety of applications, for example
 CC they may be used in profiling assays, for providing large arrays of human
 CC genetic material for implementing large-scale screening strategies and
 CC for treating diseases via gene therapy procedures

XX Sequence 455 AA;

Query Match 94.2%; Score 2283.5; DB 5; Length 455;

Best Local Similarity 98.2%; Pred. No. 3.8e-217;

Matches 439; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 MPTLLQDWCRCGEHLNTRRCMLILGIPEDCGEDBEFTLQACRHLGRYRVRIGRMFRREE 60

DB 1 MPTLLQDWCRCGEHLNTRRCMLILGIPEDCGEDBEFTLQACRHLGRYRVRIGRMFRREE 60

QY 61 NQAAILLELAQIDYALLPRIPKGGPWVIVPRNSDGEFLNRLNRFLEERTVSDM 120

DB 61 NQAAILLELAQIDYALLPRIPKGGPWVIVPRNSDGEFLNRLNRFLEERTVSDM 120

QY 121 NRVLGSDTNCAPRTVISPEFTWQAQTIGRAVQPLLEQMLYRELVRVSGNTISIPGALAF 180

DB 121 NRVLGSDTNCAPRTVISPEFTWQAQTIGRAVQPLLEQMLYRELVRVSGNTISIPGALAF 180

QY 181 DAWLEHTTEMLQMWQVPEGEKRRRLMECLRGFPALQVVSGLFASNASITVECLAAQQVF 240

DB 181 DAWLEHTTEMLQMWQVPEGEKRRRLMECLRGFPALQVVSGLFASNASITVECLAAQQVF 240

QY 241 GPVESHKIAQVKLCKAYQAGEKVSFVLRLEPLLQRAVENNVSRNVNQTRLKRVLSG 300
 DB 241 GPVESHKIAQVKLCKAYQAGEKVSFVLRLEPLLQRAVENNVSRNVNQTRLKRVLSG 300
 QY 301 ATLPDKLRDCLKLMKQRRKPPGFALVKLREEEWEATLGPDRSLRGLEVA PRPPARI 360
 DB 301 ATLPDKLRDCLKLMKQRRKPPGFALVKLREEEWEATLGPDRSLRGLEVA PRPPARI 360
 QY 361 TGVGAVPLPASGNSFDARPSQGYRRRRGRGQHRGGVARAGSRGSRKRKRTHTFCYSCGD 420
 DB 361 TGVGAVPLPASGNSFDARPSQGYRRRRGRGQHRGGVARAGSRGSRKRKRTHTFCYSCGD 420
 QY 421 GHIRVQCINPSNLLLVKQKQAAVESG 447
 DB 421 GHIRVQCINPSNLLLVKQKQAAVESG 446

RESULT 4

AAO16179
 ID AAO16179 standard; protein; 452 AA.

XX AAO16179;

XX AC AAO16179;

XX DT 28-MAR-2003 (first entry)

XX Human protein #5.

XX Human; vaccine; adult whole brain; foetal whole brain; tonsil;
 KW adult hippocampus; disease-associated SNP analysis; knockout mouse;
 KW disease model mouse; cancer; neurological disorder.

XX Homo sapiens.

XX WO200299103-A1.

XX 12-DEC-2002.

XX 27-MAY-2002; 2002WO-JP005134.

XX 04-JUN-2001; 2001JP-00168370.

XX 16-AUG-2001; 2001JP-00246915.

XX (KAZU-) KAZUSA DNA RES INST FOUND.

XX (PROT-) PROTEIN EXPRESS CO LTD.

XX Ohara O, Nagase T, Nakajima D;

XX WPI; 2003-140622/13.

XX N-PSDB; AAL51207.

XX DNA preferentially expressed in human adult and fetal brain tissue useful
 PT for diagnosis, treatment and analysis of cancer and mental disorders.

XX Claim 1; Page 56-60; 73pp; Japanese.

XX The invention comprises the amino acid and coding sequences of seven
 CC human proteins that are preferentially expressed in adult whole brain,
 CC foetal whole brain, tonsil and adult hippocampus tissue. The DNA
 CC sequences are useful for the analysis of disease-associated single
 CC nucleotide polymorphisms and the production of knockout and human disease
 CC model mice. The DNA and protein sequences of the invention are useful for
 CC the prevention (vaccine) and treatment of cancer and neurological
 CC disorders. The present amino acid sequence represents a human protein of
 CC the invention

XX Sequence 452 AA;

Query Match 36.5%; Score 883.5; DB 6; Length 452;

Best Local Similarity 42.6%; Pred. No. 2.8e-78;

Matches 201; Conservative 75; Mismatches 155; Indels 41; Gaps 10;

QY 1 MPTLLQDWCRCGEHLNTRRCMLILGIPEDCGEDBEFTLQACRHLGRYRVRIGRMFRREE 60


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PR 09-NOV-1999; 99US-0164203P.
XX (INCY-) INCYTE GENOMICS INC.
XX Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;
PI Baughn MR, Lu DAM, Patterson C;
XX WPI; 2001-169860/17.
DR N-PSDB; AAF81747.
XX Isolated polypeptide with a human membrane associated protein sequence is
XX useful for the diagnosis, prevention and treatment of cell proliferative,
XX autoimmune/inflammatory, neurological and gastrointestinal disorders.
XX Claim 1; Page 119-120; 173pp; English.
XX AAF81741 to AAF81777 encode the human membrane associated proteins
XX (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,
XX antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic and
XX antiarteriosclerotic activities, which can be used in gene therapy.
XX MEMAPs and agonist of MEMAPs can be used to treat a disease or condition
XX associated with decreased expression of functional MEMAP and antagonists
XX of MEMAP are used to treat a disease or condition associated with
XX overexpression of functional MEMAP. These disorders include cell
XX proliferative, autoimmune/inflammatory, neurological and gastrointestinal
XX disorders. The MEMAP polynucleotides and proteins are also used for the
XX diagnosis of these disorders. Specific examples of these disorders
XX include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
XX MEMAP proteins can be used to screen for compounds which specifically
XX bind MEMAP including antibodies, oligonucleotides, proteins and small
XX molecules. MEMAP polynucleotides can be used to prepare transgenic
XX animals which can be studied to provide information concerning human
XX disease. Anti-MEMAP antibodies are useful in immunoassays for the
XX detection of MEMAP protein and can be used as antagonists to treat or
XX prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
XX can be delivered to target cells with genetic abnormalities with respect
XX to the expression of MEMAP to treat or prevent a disorder associated with
XX MEMAP
XX
XX Sequence 353 AA;
Query Match 33.8%; Score 818; DB 4; Length 353;
Best Local Similarity 49.6%; Pred. No. 6e-72;
Matches 172; Conservative 52; Mismatches 113; Indels 10; Gaps 4;
QY 1 MPTLLQDWCRGEHLNTRRCMLILGIPEDCGEDEFEEETLQACRHLGRYRIGRMFRREE 60
DB 1 MAMTLLEDRCGMDVNSQRLVWGIPVNCDEAEIETLQAAAPQVS-YRMJGRMFWRREE 59
QY 61 NQAAILLEAQDIDYALLPREIPKGGPWEVIVPRNSDGEFLNRLNRFLEERRTVSDM 120
DB 60 NAKAALLELTGAVDYAAIPREMPKGGVWKVLPKPTSDAEFLRLHLFLAREGWTQDV 119
QY 121 NRVLGSDTNCAPRVTTISPEWTTWAQTLGAQVQLLEOMLYRELRFVSGNTISIPGALAF 180
DB 120 ARVLGFQNPPTTPGEPMAELNY--ILDNVIQFLVESIWYKRLTLFSGRDIPGPGETF 177
QY 181 DAWLEHTTEMLQMWQVPEGEKRRRLMECLRGPALQVWSGLNASNATVVEECALAQOVF 240
DB 178 DPWLEHTNEVLVEWQVSDVEKRRRLMESLRGPAADVIRILKSNPNPAITTAECALAEQVF 237
QY 241 GPVESHKIAQVKLCKAQAEAGEKVSFVRLRLEPLLQRAVENNVSRNNVOTRLKRVLSG 300
DB 238 GSVESSRDQAQIKFLNTYQNPGEKLSAYVIRLEPLLLQKVEKGADKDNVNOARLEQVIAG 297
QY 301 ATLDPKLRDLKLMKQRKP-PGFLALVKLLR-----EEEEEAATL 340
DB 298 ANHSGAIRRQLWLTGAGSGPAPNLFQLLVQIRBEAEKEEBEATL 344
XX
XX RESULT 7
XX AAE01340
XX ID AAE01340 standard; protein; 351 AA.
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XX AAE01340;
XX 17-JUL-2001 (first entry)
XX Human gene 22 encoded secreted protein fragment, SEQ ID NO:205.
XX Human; secreted protein; proliferative disorder; cancer; tumour;
XX foetal abnormality; developmental abnormality; haematopoietic disorder;
XX immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
XX inflammation; allergy; neurological disorder; Alzheimer's disease;
XX Parkinson's disease; cognitive disorder; schizophrenia; asthma;
XX skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
XX cardiovascular disorder; angiogenic disorder; kidney disorder;
XX gastrointestinal disorder; pregnancy-related disorder;
XX endocrine disorder; infection; wound healing; vulnerability; cell culture;
XX chemotaxis; food additive; gene therapy; binding partner identification.
XX Homo sapiens.
XX WO200134769-A2.
XX 17-MAY-2001.
XX 01-NOV-2000; 2000WO-US030040.
XX 05-NOV-1999; 99US-0163580P.
XX 30-JUN-2000; 2000US-0215130P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Komatsoulis GA, Wei P, Baker KP, Fiscella M;
XX WPI; 2001-308781/32.
XX New isolated nucleic acid molecule encoding a human secreted protein is
XX used in preventing, treating or ameliorating a medical condition.
XX Disclosure; Page 46; 519pp; English.
XX AAD05121-AAD05203 represent cDNAs corresponding to 24 human secreted
XX protein genes, and AAE01232-AAE01311 represent the proteins they encode.
XX AAE01312-AAE01340 represent human secreted protein variants or fragments.
XX The secreted proteins and their genes are useful for preventing, treating
XX or ameliorating medical conditions, e.g., by protein or gene therapy.
XX Pathological conditions can be diagnosed by determining the amount of the
XX new protein in a sample or by determining the presence of mutations in
XX the new genes. Specific uses are described for each of the 24 genes,
XX based on the tissues in which they are most highly expressed, and include
XX developing products for the diagnosis or treatment of proliferative
XX disorders, cancer, tumours, foetal and developmental abnormalities,
XX haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
XX diseases (e.g., rheumatoid arthritis), inflammation, allergies,
XX neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
XX cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
XX psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
XX angiogenic disorders, kidney disorders, gastrointestinal disorders,
XX pregnancy-related disorders, endocrine disorders, and infections. The
XX proteins can also be used to aid wound healing and epithelial cell
XX proliferation, to prevent skin aging due to sunburn, to maintain organs
XX before transplantation, for supporting cell culture of primary tissues,
XX to regenerate tissues, to identify their cognate ligands or binding
XX partners, and in chemotaxis, and can be used as a food additive or
XX preservative to modify storage properties. Antibodies specific for a
XX protein of the invention can be used in alleviating symptoms associated
XX with the disorders mentioned above, and in diagnostic immunoassays e.g.,
XX radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
XX present sequence represents a human secreted protein fragment referred to
XX in the disclosure of the invention
XX Sequence 351 AA;
Query Match 31.7%; Score 768.5; DB 4; Length 351;
```


PN WO200168851-A2.
 XX 20-SEP-2001.
 XX 12-MAR-2001; 2001WO-US007735.
 XX 10-MAR-2000; 2000US-0188277P.
 XX 10-MAR-2000; 2000US-0188316P.
 PR 14-MAR-2000; 2000US-0189139P.
 PR 14-MAR-2000; 2000US-0189140P.
 PR 17-MAR-2000; 2000US-0190231P.
 PR 17-MAR-2000; 2000US-0190401P.
 XX (CURA-) CURAGEN CORP.
 XX Padigar M, Vernet CAM, Fernandes E, Shimkets RA, Spaderna SK;
 PI Majumder K, Li L;
 XX WPI; 2001-570869/64.
 DR N-PSDB; AAS13342.
 XX Novel polypeptides and nucleic acids homologous to members of collagen,
 PT potassium channel, tuftelin family of proteins for diagnosing, treating
 PT cancer, atherosclerosis, neurological, skin and enamel defect disorders.
 XX Claim 1; Page 29; 128pp; English.
 XX The invention relates to isolated NOVX (NOVX1-11) polypeptides and the
 CC polynucleotides that encode them. NOVX polypeptides, polynucleotides and
 CC anti-NOVX antibodies are useful for treating or preventing a pathology
 CC associated with NOVX polypeptide in humans and for treating a syndrome
 CC associated with human disease e.g. disorders characterised by altered
 CC cell motility, proliferation and migration e.g. cancer, angiogenesis and
 CC wound healing (NOV1-3), neurological disorders, e.g. episodic ataxia,
 CC autosomal dominant myokymia, stroke, Parkinson's disease, Alzheimer's
 CC disease, non-insulin dependent diabetes mellitus, asthma, hypertension
 CC and seizure (NOV4), enamel defects, such as amelogenesis imperfecta and
 CC disorders involving enamel defects, including hypoplasia and
 CC hypomineralisation (NOV5-7), paraneoplastic neurological disorders, e.g.
 CC paraneoplastic limbic of brain-stem encephalitis occurring during
 CC testicular cancer, diabetes, reproductive health, metabolic and endocrine
 CC disorders, gastrointestinal disorders, immune disorders and autoimmune
 CC diseases, respiratory disorders, bone disorders, musculoskeletal
 CC disorders, leukaemia/lymphoma and tissue/cell growth regulation disorders
 CC (NOV8), lesional psoriatic skin (NOV9-10) and atherosclerosis, abdominal
 CC aortic aneurysm and neurological disorders (NOV11). NOVX polypeptide is
 CC also useful for identifying an agent that binds to it and a cell
 CC expressing NOVX polypeptide is useful for identifying a therapeutic agent
 CC for use in treatment of a NOVX related pathology. The antibodies and a
 CC polypeptide having 95% sequence identity to NOVX polypeptide are useful
 CC for treating a pathological state in a mammal. The present sequence
 CC represents NOV8, a possible neuronal antigen-like protein
 XX Sequence 351 AA;
 Query Match 31.7%; Score 768.5; DB 4; Length 351;
 Best Local Similarity 46.6%; Pred. No. 4.8e-67;
 Matches 165; Conservative 60; Mismatches 118; Indels 11; Gaps 6;
 QY 1 MPTLLQDWCRCGHEHLNTRCMLILGIPEDCGDEFEETLQACRHLGRYVIGMFRREE 60
 DB 1 MTELELDWCRCGMDNPRKALLIAGISQSCVAIEALQALGAPLGEYRLLLGNFRDE 60
 QY 61 NAKAILLEAQDIDYALLPREIPCKGPGPWEIVKPRNSDGEFLNRLNRFLEERRTYSDM 120
 DB 61 NRKVALVLTAEETHALVPKEIPKGGIWRVIFKPPDPDNTFLSLNFELEGMTVGEL 120
 QY 121 NRVLGSDTNCSPRVTISPEFWT--WAQTLGAAVQPLLEQMLYRELVRVFSGNTTISIPGAL 178
 DB 121 SRALGHENGSLDPEQGMPEWAPMLAQAL-EALQPALQCLKYLKRVFSGRESPEEGEE 179
 QY 179 AFDALWLEHTTLMQWQPEKGRRLMECLRGALQVVSGLRASNASITVEECIALQ 238
 DB 179 AFDALWLEHTTLMQWQPEKGRRLMECLRGALQVVSGLRASNASITVEECIALQ 238
 DB 180 EFGRWMEHTTQMIKAWQVDPDVEKRRLLESRLGSPALDVIRVLKINNPLITVDECLQALEE 239
 QY 239 VFGPVESHKIAQVKLCYQAGEKVSFVLEPLLOPRAVENNVYRRNVQTRLKRVL 298
 DB 240 VFGVTDNPRELQVKYLTYYQDEEKLSAYVLEPLLOKLVQVGAERDAVNOARLDQVI 299
 QY 299 SGATLPDKLRDKLKMQRKPPGFALVKLRE---EEWEATLPGDRESLEG 349
 DB 300 AGA-VHKTIIRRELNL-PEDGPAPGFLQLLVLIKDYEAEEEEALL---QAILEG 348
 RESULT 10
 ADA54410
 ID ADA54410 standard; protein; 399 AA.
 XX ADA54410;
 AC AC
 XX 20-NOV-2003 (first entry)
 DT
 XX Human protein, SEQ ID 1978.
 DE
 XX Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
 KW inflammatory disease; osteoporosis; neurological disease.
 XX Homo sapiens.
 OS
 XX EP1293569-A2.
 PN
 XX 19-MAR-2003.
 PD
 XX 21-MAR-2002; 2002BP-00006586.
 PF
 XX 14-SEP-2001; 2001JP-00328381.
 XX
 PR 24-JAN-2002; 2002US-0350435P.
 PR
 XX (HELI-) HELIX RES INST.
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 PA
 XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX WPI; 2003-395539/38.
 XX N-PSDB; ADA52771.
 DR
 XX New polynucleotides encoding full-length polypeptides, e.g. secretory
 PT and/or membrane proteins, useful for developing medicines for diseases in
 PT which the gene is involved, or as target molecules for gene therapy.
 XX Claim 14; SEQ ID NO 1978; 205pp; English.
 XX The present invention relates to novel human secretory or membrane
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
 CC ADA54071). The coding sequences are useful in the gene therapy of
 CC diseases caused by abnormalities of the proteins, e.g. cancer,
 CC inflammatory diseases, osteoporosis or neurological disease.
 XX Sequence 399 AA;
 Query Match 31.7%; Score 768.5; DB 6; Length 399;
 Best Local Similarity 42.5%; Pred. No. 5.9e-67;
 Matches 171; Conservative 72; Mismatches 130; Indels 29; Gaps 7;
 QY 1 MPTLLQDWCRCGHEHLNTRCMLILGIPEDCGDEFEETLQACRHLGRYVIGMFRREE 60
 DB 1 MAVTMLQDWCRCGWNARRGLLIIGIPEDCDDAEFQBSLEAALRPMGHFTVLGKAFREED 60
 QY 61 NAKAILLEAQDIDYALLPREIPCKGPGPWEIVKPRNSDGEF--LNLNRFLEERRTVS 118
 DB 61 NATAAVELDREVNVALVPREIPGTGGPWNVVFPRCSGEEFLGLGRVFFHPEQEGQWVE 120
 QY 119 DMNRVLGSDTNCSPRVTISPEFWTNAQTLGAAVQPLLEQMLYRELVRVFSGNTTISIPGAL 178

Db 121 SVAGALG-----VGLRRV-----CWLRSIGAVQVPWVEAVRCQSLGVTSGRDQAPGEE 169
 QY 179 AFDWLEHTTEMLQMWQ-VPEGEKRRRLMECLRGPALQVVGSLRASNASITVEECALAQ 237
 Db 170 SPEVWLDHTTEMLHVWQGVSERRRRRLLEGLRGTAQLVHALLAENPARTAQDCUAA 229
 QY 238 QVFGPVESHKIAQVKLCCKAYQAGEKVVSVFLRLEPLQLQRAVENNVVSRNNVNOTLKV 297
 Db 230 QVFGDNESQATIRVKCLTAQQSGEELSAFVLRLVLLQKAMEKEALASADRVLQRM 289
 QY 298 LSGATLPDKLRDKLKMQRKPPGPIALVKLLRBEWEATLG----PDRESLEGEVA 353
 Db 290 LTRAHLTEPLDALRKLRMAGRSPSFLEMLGLVRESEAWESLARSVRAQTQEGAGARAG 349
 QY 354 PRPPARI-TGVGAVP-----LPASGNSFDARPSQGYR 384
 Db 350 AQAVARASTKVEAVPGGPREPEGLLQAGQAEELLQEGLK 391

RESULT 11

ABG99947
 ID ABG99947 standard; protein; 399 AA.

AC ABG99947;

DT 17-JAN-2003 (first entry)

DE Human novel polypeptide #60.

KW Human; genetic disorder; gene mapping; medical imaging; cancer;
 KW neurodegenerative disorder; lymphoid cell disorder; osteoporosis;
 KW Parkinson's disease; Alzheimer's disease; bone degenerative disorder;
 KW osteoarthritis; periodontal disease; liver fibrosis; viral infection;
 KW fungal infection; bacterial infection; autoimmune disease; diabetes;
 KW atopic dermatitis.

XX Homo sapiens.

XX WO200274961-A1.

XX 26-SEP-2002.

PF 14-MAR-2002; 2002MO-US005109.

PR 15-MAR-2001; 2001US-00810173.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Zhou P, Goodrich R, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Drmanac RT;

DR WPI; 2003-040556/03.
 DR N-PSDB; ABX05045.

XX New isolated polypeptides and polynucleotides, useful for preventing,
 PT treating or ameliorating medical conditions, such as cancer,
 PT neurodegenerative disorders, lymphoid cell disorders, bone degenerative
 PT disorders, and infections.

XX Claim 9; SEQ ID NO 586; 235pp; English.

XX The invention relates to human polynucleotides and the polypeptides they
 CC encode. The polynucleotides and polypeptides are useful in diagnostics,
 CC forensics, gene mapping, medical imaging, identification of mutations,
 CC responsible for genetic disorders or other traits, assessing biodiversity
 CC and producing many other types of data and products dependent on DNA and
 CC amino acid sequences. They are also useful for preventing, treating or
 CC ameliorating medical conditions, such as cancer, neurodegenerative
 CC disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell
 CC disorders, osteoporosis, osteoarthritis, bone degenerative disorders,
 CC periodontal disease, liver fibrosis, infections (e.g. viral, fungal or

CC bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis).
 CC Sequences ABG9988-ABG9989 and ABU00010-ABU00433 represent human
 CC polypeptides of the invention. Note: the sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied by the European Patent Office
 XX
 SQ Sequence 399 AA;

Query Match 31.7%; Score 768.5; DB 6; Length 399;

Best Local Similarity 42.5%; Pred. No. 5.9e-67;

Matches 171; Conservative 72; Mismatches 130; Indels 29; Gaps 7;

QY 1 MPTLLQDWCRGHEHLNTRRCMLILGIPEDCGDEFEETLQEAQRHLGVRVLTGRMFRER 60

Db 1 MAVTWLQDWCRWGVNARGLILGIPEDCDAEQESLEAALRPMGHFTVLGKAPRED 60

QY 61 NQAQILLELAQDIDYALLPREIPGKGPWEVIVKPNSDGEF--LNRLNRFLEEEERTVS 118

Db 61 NATAALVELDREVNVALVPREIPGTGGPNVVFVPRCSGEFGLGLGRVFFHPEQEGQVVE 120

QY 119 DMNRVLGSDTNCASAPRVTISPFWTWAQTLGAQVQPLLEQMLYRELVRVFSNGTISIPGAL 178

Db 121 SVAGALG-----VGLRRV-----CWLRSIGAVQVPWVEAVRCQSLGVTSGRDQAPGEE 169

QY 179 AFDWLEHTTEMLQMWQ-VPEGEKRRRLMECLRGPALQVVGSLRASNASITVEECALAQ 237

Db 170 SPEVWLDHTTEMLHVWQGVSERRRRRLLEGLRGTAQLVHALLAENPARTAQDCUAA 229

QY 238 QVFGPVESHKIAQVKLCCKAYQAGEKVVSVFLRLEPLQLQRAVENNVVSRNNVNOTLKV 297

Db 230 QVFGDNESQATIRVKCLTAQQSGEELSAFVLRLVLLQKAMEKEALASADRVLQRM 289

QY 298 LSGATLPDKLRDKLKMQRKPPGPIALVKLLRBEWEATLG----PDRESLEGEVA 353

Db 290 LTRAHLTEPLDALRKLRMAGRSPSFLEMLGLVRESEAWESLARSVRAQTQEGAGARAG 349

QY 354 PRPPARI-TGVGAVP-----LPASGNSFDARPSQGYR 384

Db 350 AQAVARASTKVEAVPGGPREPEGLLQAGQAEELLQEGLK 391

RESULT 12

AAAB12525

ID AAAB12525 standard; protein; 329 AA.

AC AAAB12525;

XX 02-NOV-2000 (first entry)

XX Human Mal protein SEQ ID NO:4.

XX Mal1, Mal2; Mal3; Mal4; Mal5; paraneoplastic limbic encephalitis; diagnosis;
 KW paraneoplastic syndrome; neoplasm; colon cancer; brainstem encephalitis;
 KW breast cancer; parotid gland cancer; lung cancer; testicular cancer;
 KW germ-cell tumour.

XX Homo sapiens.

XX JP2000146982-A.

XX 26-MAY-2000.

XX 10-NOV-1999; 99JP-00320171.

XX 10-NOV-1998; 98US-00189527.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX WPI; 2000-468119/41.

XX N-PSDB; AAA60833.

XX Diagnosing paraneoplastic syndrome e.g. paraneoplastic limbic
 PT encephalitis or neoplasm e.g. colon cancer comprising assessing a test

PT sample for the presence or absence of antibodies to a Ma family
 PT polypeptide.

XX Claim 48; Fig 1; 27pp; Japanese.

XX The present invention describes a method for diagnosing a paraneoplastic
 CC syndrome or neoplasm. The method comprises assessing a test sample for the
 CC presence or absence of antibodies to a Ma family polypeptide (I). The
 CC method is used to diagnose a paraneoplastic syndrome especially
 CC paraneoplastic limbic encephalitis and/or brainstem encephalitis or
 CC neoplasm in an individual. The method diagnoses the neoplasm by assessing
 CC antibodies to (I) preferably Ma1, which is indicative presence of breast
 CC cancer, colon cancer, parotid gland cancer, lung cancer, testicular
 CC cancer, and germ-cell tumours or Ma2, which is indicative of testicular
 CC cancer, germ-cell tumour, and lung cancer. The present sequence is the
 CC Ma1 protein as given in the present invention

XX Sequence 329 AA;

Query Match 31.2%; Score 755.5; DB 3; Length 329;
 Best Local Similarity 48.8%; Pred. No. 8.5e-66;
 Matches 156; Conservative 50; Mismatches 111; Indels 3; Gaps 2;
 QY 1 MPTLLQDWCRGHEHLNTRRCMLILGIPDCGDEFEETLOEACRHLGRYVIGRMFRRE 60
 DB 1 MAMTLEDWCRGMDVNSQRILLVWGIPVNCDEAEIETLQAMQVS-YRMLGRMFRRE 59
 QY 61 NQAAILLELAQIDYALLPREIPKGGPWVIVKPRNSDGEFLNRLNRFLEERRTVSDM 120
 DB 60 NAKAALDELTAQVDAAPREMPKGGVWVLPKPTSDAEFLERLHLLAREGWTQDV 119
 QY 121 NRVLGSDTNCAPRVVISPEFWTQAOTLGAQVPLLEOMLYRELRFVSGNTISIPGALF 180
 DB 120 ARVLGFQNPFTPGPMPAEMLYN-ILDNVIOPLVESIWYKRLTFSFGHPRAWGNF 177
 QY 181 DAMEHTEMLQMWQVPEGKRRRLMELRGPAQVQVSGLRASNASITVECLAAQOVF 240
 DB 178 DPWLEHNEVLEWQVSDVEKTRLMESLRGPAADVIRLKSNPAITAECLALEHVP 237
 QY 241 GPVESHKIAQVKLCKAYOAGEKVSFVLRLPLQLRAVENNVSRNNVQTRKRVLSG 300
 DB 238 GSVESSRDAQIKFLNTYQNPGEKLSAYVIRLEPLQKVKGEAIDKDNVQARLEQVIAG 297
 QY 301 ATLPDLKRLDKLMKQRKP 320
 DB 298 ANHSGAIRQLWLTGAREGP 317

RESULT 13

AAB43023
 ID AAB43023 standard; protein; 312 AA.

XX AAB43023;

XX 08-FEB-2001 (first entry)

DE Human ORFX ORF2787 polypeptide sequence SEQ ID NO:5574.

XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive.

OS Homo sapiens.
 XX WO200058473-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US008621.

XX 31-MAR-1999; 99US-0127607P.

XX 02-APR-1999; 99US-0127636P.

XX 05-APR-1999; 99US-0127728P.

XX 30-MAR-2000; 2000US-00540763.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2000-602362/57.

XX N-PSDB; AAC77232.

XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease.

XX Claim 11; Page 4759; 5507pp; English.

XX AAB74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
 CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
 CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
 CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
 CC antiviral; antifungal; antirheumatic; antithyroid; and antianemic. The
 CC sequences can be used for determining the presence of or predisposition
 CC to, or preventing or treating pathological conditions associated with an
 CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be
 CC used to treat cancers, proliferative disorders, neurodegenerative
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
 CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive

XX Sequence 312 AA;

Query Match 30.6%; Score 740.5; DB 3; Length 312;

Best Local Similarity 48.8%; Pred. No. 2.4e-64;

Matches 148; Conservative 51; Mismatches 101; Indels 3; Gaps 2;

QY 1 MPTLLQDWCRGHEHLNTRRCMLILGIPDCGDEFEETLOEACRHLGRYVIGRMFRRE 60

DB 1 MTLRLLEDWCRGMDMNPCKALLIAGISQSCVAIEEALQAGLAPLGEYLLGRMFRDE 60

QY 61 NQAAILLELAQIDYALLPREIPKGGPWVIVKPRNSDGEFLNRLNRFLEERRTVSDM 120

DB 61 NRKVALVGLTAETSHALVPKEIPKGGIWRVIFKPPDPDNTFLSRLNEFLAGEGMTVGL 120

QY 121 NRVLGSDTNCAPRVVISPEFWT--QAOTLGAQVPLLEOMLYRELRFVSGNTISIPGAL 178

DB 121 SRALGHENGSLDPEQGMIPEMWAPMLAQAAL-EALQALQCLKYKKLVFSGRSPPEGEE 179

QY 179 AFDALWHTTEMLQMWQVPEGKRRRLMELRGPAQVQVSGLRASNASITVECLAAQO 238

DB 180 EFGWPHHTTQMLNAQVDPVDEKRRRLLESRLGPAADVIRVLKINNPLITVDECLQALEE 239

QY 239 VFGVESHKIAQVKLCKAYOAGEKVSFVLRLPLQLRAVENNVSRNNVQTRKRVLSG 298

DB 240 VFGVTDNPRELQVKYLLTTYQKDEKLSAYVLRLEPLQLKLVQGAERDAVNQARLDQVI 299

```

QY 299 SGA 301
   :||
Db 300 AGA 302

RESULT 14
AAB12528
ID AAB12528 standard; protein; 283 AA.
XX
AC AAB12528;
XX
DT 02-NOV-2000 (first entry)
XX
DE Human Ma4 protein SEQ ID NO:11.
XX
KW Ma1; Ma2; Ma3; Ma4; Ma5; paraneoplastic limbic encephalitis; diagnosis;
KW paraneoplastic syndrome; neoplasm; colon cancer; brainstem encephalitis;
KW breast cancer; parotid gland cancer; lung cancer; testicular cancer;
KW germ-cell tumour.
XX
OS Homo sapiens.
XX
PN JP2000146982-A.
XX
PD 26-MAY-2000.
XX
PF 10-NOV-1999; 99JP-00320171.
XX
PR 10-NOV-1998; 98US-00189527.
XX
(SLOK ) SLOAN KETTERING INST CANCER RES.
PA
DR WPI: 2000-468119/41.
DR N-PSDB; AAB60836.
XX
PT Diagnosing paraneoplastic syndrome e.g. paraneoplastic limbic
PT encephalitis or neoplasm e.g. colon cancer comprising assessing a test
PT sample for the presence or absence of antibodies to a Ma family
PT polypeptide.
XX
PS Claim 48; Fig 7-8; 27pp; Japanese.
XX
CC The present invention describes a method for diagnosing a paraneoplastic
CC syndrome or neoplasm. The method comprises assessing a test sample for
CC the presence or absence of antibodies to a Ma family polypeptide (I). The
CC method is used to diagnose a paraneoplastic syndrome especially
CC paraneoplastic limbic encephalitis and/or brainstem encephalitis or
CC neoplasm in an individual. The method diagnoses the neoplasm by assessing
CC antibodies to (I) preferably Ma1, which is indicative presence of breast
CC cancer, colon cancer, parotid gland cancer, lung cancer, testicular
CC cancer and germ-cell tumours or Ma2, which is indicative of testicular
CC cancer, germ-cell tumour, and lung cancer. The present sequence is the
CC Ma4 protein as given in the present invention
XX
SQ Sequence 283 AA;
   Query Match      25.5%; Score 617.5; DB 3; Length 283;
   Best Local Similarity 50.2%; Pred. No. 3 3e-52;
   Matches 135; Conservative 44; Mismatches 85; Indels 5; Gaps 3;

QY 82 IPGKGPPWEIVKPNSSGEFNLNRLNRLFLLEERTVSDMNRVLGSDTNCAPRVTTISPEF 141
Db 1 VQGGGVKVKVFKTPNQDTFLERLNLFLEKEGQTVSGMFRALGQGVSPATVPCISPEL 60
QY 142 WT--WAOTLGAQVPLLEQMLYRELVRVSGNTISIPGALAPDAWLEHTTEMLQWQVPEG 199
Db 61 LAHLGQAWAPQPLL--PMRYRKURVFGSGAVPAPEEDSFVWLEQATEIVKWEFVTEA 119
QY 200 EKRRIMECLRGFALQVSGLRASNASITVECLAAQVFGPVESHKIAQVKLCKAYQE 259
Db 120 EKRWLAESLRGALDLHIVQADNPSISVEECLAFKQVFGSLRSRRTAQVRYLKTQVE 179
QY 260 AGEKSSVFVRLPLELLQRAVENNVSVRRNVNTRLKRVLSGATLPDKLRDKLKMQRKK 319

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Db 180 EGEKVSAYVLRLETLRLKRAVEKRAIPRIADQVRLEQVMAGATLQMLWLCRLRELKQGP 239
 QY 320 PFGFALVKLREBEWEATLQPDRESUE 348
 Db 240 PPSFLELMKVIREEEESASF--ENESIE 266

RESULT 15
 AAE01336
 ID AAE01336 standard; protein; 280 AA.
 XX
 AC AAE01336;
 XX
 DT 17-JUL-2001 (first entry)
 XX
 DE Human gene 22 encoded secreted protein fragment, SEQ ID NO:201.
 XX
 KW Human; secreted protein; proliferative disorder; cancer; tumour;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder;
 KW endocrine disorder; infection; wound healing; vulnery; cell culture;
 KW chemotaxis; food additive; gene therapy; binding partner identification.
 XX
 OS Homo sapiens.
 XX
 PN WO200134769-A2.
 XX
 PD 17-MAY-2001.
 XX
 PF 01-NOV-2000; 2000WO-US030040.
 XX
 PR 05-NOV-1999; 99US-0163580P.
 PR 30-JUN-2000; 2000US-0215130P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Komatsoulis GA, Wei P, Baker KP, Fiscella M;
 DR WPI: 2001-308781/32.
 XX
 PT New isolated nucleic acid molecule encoding a human secreted protein is
 PT used in preventing, treating or ameliorating a medical condition.
 XX
 PS Disclosure; Page 46; 519pp; English.

AAD05121-AAD05203 represent cDNAs corresponding to 24 human secreted
 protein genes, and AAE01332-AAE01311 represent the proteins they encode.
 AAE01312-AAE01340 represent human secreted protein variants or fragments.
 The secreted proteins and their genes are useful for preventing, treating
 or ameliorating medical conditions, e.g. by protein or gene therapy.
 Pathological conditions can be diagnosed by determining the amount of the
 new protein in a sample or by determining the presence of mutations in
 the new genes. Specific uses are described for each of the 24 genes,
 based on the tissues in which they are most highly expressed, and include
 developing products for the diagnosis or treatment of proliferative
 disorders, cancer, tumours, foetal and developmental abnormalities,
 haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
 diseases (e.g. rheumatoid arthritis), inflammation, allergies,
 neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
 cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
 psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
 angiogenic disorders, kidney disorders, gastrointestinal disorders,
 pregnancy-related disorders, endocrine disorders, and infections. The
 proteins can also be used to aid wound healing and epithelial cell
 proliferation, to prevent skin aging due to sunburn, to maintain organs
 before transplantation, for supporting cell culture of primary tissues,
 to regenerate tissues, to identify their cognate ligands or binding

Blank

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OM protein - protein search, using sw model

Run on: September 27, 2004, 17:05:06 ; Search time 18.7467 Seconds
(without alignments)
2507.755 Million cell updates/sec

Title: US-10-037-860-9
Perfect score: 766
Sequence: 1 DLMHIVQADNPISVBECLF.....SIEPERDGYGRWNHGGDD 149

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	766	100.0	149	4	Q9UL43	Q9UL43 homo sapien
2	758	99.0	364	4	Q94959	Q94959 homo sapien
3	755	98.6	283	4	Q9UL42	Q9UL42 homo sapien
4	741	96.7	364	6	Q9GMU3	Q9GMU3 macaca fasc
5	600.5	78.4	365	11	Q8BHK0	Q8BHK0 mus musculu
6	323.5	42.2	466	11	Q8JZW8	Q8JZW8 mus musculu
7	323	42.2	455	4	Q9H0A4	Q9H0A4 homo sapien
8	323	42.2	463	4	Q9UL41	Q9UL41 homo sapien
9	295.5	38.6	192	4	Q8ND90	Q8ND90 homo sapien
10	295.5	38.6	353	4	Q95144	Q95144 homo sapien
11	295.5	38.6	353	4	Q8NG07	Q8NG07 homo sapien
12	294.5	38.4	353	11	Q8VHZ4	Q8VHZ4 rattus norv
13	287	37.5	448	4	Q8NET3	Q8NET3 homo sapien
14	287	37.5	452	4	Q96PV4	Q96PV4 homo sapien
15	285.5	37.3	353	11	Q9CYP2	Q9CYP2 mus musculu
16	285.5	37.3	353	11	Q8C1C8	Q8C1C8 mus musculu

17	277	36.2	399	4	Q96A40	Q96A40 homo sapien
18	274	35.8	351	6	Q95KI4	Q95KI4 macaca fasc
19	271.5	35.4	351	4	Q96BY2	Q96BY2 homo sapien
20	266.5	34.8	237	4	Q9H833	Q9H833 homo sapien
21	266.5	34.8	351	4	Q9HAS1	Q9HAS1 homo sapien
22	257.5	33.6	352	11	Q9ERH6	Q9ERH6 mus musculu
23	250	32.6	402	11	Q9CZA5	Q9CZA5 mus musculu
24	247.5	32.3	403	4	Q8TE36	Q8TE36 homo sapien
25	245	32.0	393	11	Q9DBI7	Q9DBI7 mus musculu
26	245	32.0	393	11	Q8VD24	Q8VD24 mus musculu
27	237	30.9	402	4	Q8NIC1	Q8NIC1 homo sapien
28	100.5	13.1	386	4	Q8TCR7	Q8TCR7 homo sapien
29	98.5	12.9	525	11	Q80VR9	Q80VR9 mus musculu
30	97.5	12.7	218	4	Q9BT43	Q9BT43 homo sapien
31	97.5	12.7	225	11	Q8ROC0	Q8ROC0 mus musculu
32	97.5	12.7	543	4	Q8IU72	Q8IU72 homo sapien
33	92	12.0	185	16	Q8DE96	Q8DE96 vibrio vuln
34	92	12.0	286	16	Q8RG59	Q8RG59 fusobacteri
35	90.5	11.8	582	13	Q7ZU09	Q7ZU09 brachydanio
36	90	11.7	543	11	Q8KOZ0	Q8KOZ0 mus musculu
37	90	11.7	567	3	Q9UUS7	Q9UUS7 collatotic
38	90	11.7	592	4	Q9UJT2	Q9UJT2 homo sapien
39	89.5	11.7	218	11	Q9DBG0	Q9DBG0 mus musculu
40	89.5	11.7	471	10	Q93YN7	Q93YN7 arabidopsis
41	89.5	11.7	760	10	Q8VZU7	Q8VZU7 arabidopsis
42	89.5	11.7	800	4	O43290	O43290 homo sapien
43	89.5	11.7	1280	12	Q8QTF6	Q8QTF6 white spot
44	89	11.6	806	11	Q9Z314	Q9Z314 rattus norv
45	88.5	11.6	562	13	Q7SZP4	Q7SZP4 brachydanio

ALIGNMENTS

RESULT 1

Q9UL43	PRELIMINARY;	PRT;	149 AA.
AC	Q9UL43		
DT	01-MAY-2000 (TREMREL. 13, Created)		
DT	01-MAY-2000 (TREMREL. 13, Last sequence update)		
DT	01-MAY-2000 (TREMREL. 13, Last annotation update)		
DE	Paraneoplastic cancer-testis-brain antigen (Fragment).		
GN	MA3.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Gultekin S.H., Voltz R., Rosenfeld M.R., Gerstner E., Eichen J.,		
RA	Posner J.B., Dalmay J.;		
RT	"Identification of a novel cancer testis brain antigen using serum		
RT	antibodies from patients with testicular tumors and paraneoplastic		
RT	limbic encephalomyelitis.";		
RL	Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF083114; AAF05625.1; -		
FT	NON TER		
SQ	SEQUENCE 149 AA; 17421 MW; D46136701D3C5651 CRC64;		

Query Match 100.0%; Score 766; DB 4; Length 149;
Best Local Similarity 100.0%; Pred.No. 9.1e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	DLMHIVQADNPISVBECLFQVFGSLERRTAQVRLKPYQEEGKVSAYVLRLETL	60
Db	1	DLMHIVQADNPISVBECLFQVFGSLERRTAQVRLKPYQEEGKVSAYVLRLETL	60
Qy	61	LRRAVEKRAIPRIADQVRLQVMAQTINQMLWCLRELKQGGPPSPFLELMKVIREEE	120
Db	61	LRRAVEKRAIPRIADQVRLQVMAQTINQMLWCLRELKQGGPPSPFLELMKVIREEE	120
Qy	121	EEEASFENESIEPERDGYGRWNHGGDD	149

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Db      121 EEEASFENESIEPEERDGYGRWNHEGDD 149

RESULT 2
O94959 PRELIMINARY; PRT; 364 AA.
AC O94959;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein KIAA0883 (Paraneoplastic associated brain-testis-
DE cancer antigen).
GN KIAA0883.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K., Suyama H., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:335-364(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Eichen J.G., Dalmay J., Wade D., Rosenfeld M.R.;
RT "Characterization of a Brain-Testis-Cancer Antigen.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB020690; BAA74906.1; -.
DR EMBL; AF286487; AAG28165.1; -.
DR Genew; HGNC:9159; PNMA2.
DR InterPro; IPR005162; Retrotrans_gag.
DR Pfam; PF03732; Retrotrans_gag; 1.
KW Hypothetical protein.
SQ SEQUENCE 364 AA; 41509 MW; 6E417AD96B3F0E93 CRC64;

Query Match 99.0%; Score 758; DB 4; Length 364;
Best Local Similarity 99.3%; Pred. No. 1.3e-60;
Matches 148; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMHIVQADNPISIVVEECLEAFKQVFGSLESRTAQVRLKPYQEEGKVSAYVLETL 60
Db 216 DLMHIVQADNPISIVVEECLEAFKQVFGSLESRTAQVRLKPYQEEGKVSAYVLETL 275

QY 61 LRRAVEKRAIPRIADQVRLQVMAQATLNQMLWCLRELKDGQPPPSFLELMKVIREEE 120
Db 276 LRRAVEKRAIPRIADQVRLQVMAQATLNQMLWCLRELKDGQPPPSFLELMKVIREEE 335

QY 121 EEEASFENESIEPEERDGYGRWNHEGDD 149
Db 336 EEEASFENESIEPEERDGYGRWNHEGDD 364

RESULT 3
Q9UL42 PRELIMINARY; PRT; 283 AA.
AC Q9UL42;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Paraneoplastic cancer-testis-brain antigen (Fragment).
GN MA4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gultekin S.H., Voltz R., Rosenfeld M.R., Gerstner E., Eichen J.,

```

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RA Posner J.B., Dalmay J.;
RT "Identification of a novel cancer testis brain antigen using serum
RT antibodies from patients with testicular tumors and paraneoplastic
RT limbic encephalomyelitis.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF083115; AAF05626.1; -.
DR InterPro; IPR005162; Retrotrans_gag.
DR Pfam; PF03732; Retrotrans_gag; 1.
FT NON_TER 1
SQ SEQUENCE 283 AA; 32333 MW; E27BA6BCDCD240A4 CRC64;

Query Match 98.6%; Score 755; DB 4; Length 283;
Best Local Similarity 98.7%; Pred. No. 1.9e-60;
Matches 147; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMHIVQADNPISIVVEECLEAFKQVFGSLESRTAQVRLKPYQEEGKVSAYVLETL 60
Db 135 DLMHIVQADNPISIVVEECLEAFKQVFGSLESRTAQVRLKPYQEEGKVSAYVLETL 194

QY 61 LRRAVEKRAIPRIADQVRLQVMAQATLNQMLWCLRELKDGQPPPSFLELMKVIREEE 120
Db 195 LRRAVEKRAIPRIADQVRLQVMAQATLNQMLWCLRELKDGQPPPSFLELMKVIREEE 254

QY 121 EEEASFENESIEPEERDGYGRWNHEGDD 149
Db 255 EEEASFENESIEPEERDGYGRWNHEGDD 283

RESULT 4
Q9GMU3 PRELIMINARY; PRT; 364 AA.
AC Q9GMU3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047632; BAB12156.1; -.
DR InterPro; IPR005162; Retrotrans_gag.
DR Pfam; PF03732; Retrotrans_gag; 1.
KW Hypothetical protein.
SQ SEQUENCE 364 AA; 41350 MW; 0CF72210D7EC1524 CRC64;

Query Match 96.7%; Score 741; DB 6; Length 364;
Best Local Similarity 97.3%; Pred. No. 4.7e-59;
Matches 145; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLMHIVQADNPISIVVEECLEAFKQVFGSLESRTAQVRLKPYQEEGKVSAYVLETL 60
Db 216 DLMHIVQADNPISIVVEECLEAFKQVFGSLESRTAQVRLKPYQEEGKVSAYVLETL 275

QY 61 LRRAVEKRAIPRIADQVRLQVMAQATLNQMLWCLRELKDGQPPPSFLELMKVIREEE 120
Db 276 LRRAVEKRAIPRIADQVRLQVMAQATLNQMLWCLRELKDGQPPPSFLELMKVIREEE 335

QY 121 EEEASFENESIEPEERDGYGRWNHEGDD 149
Db 336 EEEASFENESIEPEERDGYGRWNHEGDD 364

RESULT 5

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Q8BHK0
ID Q8BHK0 PRELIMINARY; PRT; 365 AA.
AC Q8BHK0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to KIAA0883 protein.
DE PMA2 OR A830049P17RIK.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR ENBL; AK043718; BAC31626.1; -
DR ENBL; AK043910; BAC31700.1; -
DR MGD; MGI:2444129; Pma2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000425; MIP.
DR InterPro; IPR005162; Retrotrans_gag.
DR Pfam; PF03732; Retrotrans_gag; 1.
DR PROSITE; PS00221; MIP; 1.
SQ SEQUENCE 365 AA; 41201 MW; 0F90C940B9D843D9 CRC64;

Query Match 78.4%; Score 600.5; DB 11; Length 365;
Best Local Similarity 82.2%; Pred. No. 2.5e-46;
Matches 120; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

QY 1 DLHIVQADNPISVVECLEAFKQVFGSLESRRTAQVRYLKPQYEGEKVSAYVLRLETL 60
Db 216 DLHIVQADNPISVSGCLEAFKQVFGSTESRRTSQVKLYRTYQOGEKISAYVLRLETL 275

QY 61 LRAVEKRAIPRRADQVRLEQVMAGATLNQMLWCRLELKDQGGPPSPFLMLKVIREEE 120
Db 276 LRAVEKRAIPRRADQVRLEQVMAGANLGNVLWCRLELKDQGLPTFLQMLKVIREEE 335

QY 121 EEE-ASPENSIIEPREDGVRWNH 145
Db 336 EEDAYPEQESREPFREGSGCWN 361

RESULT 6
Q8JZW8
ID Q8JZW8 PRELIMINARY; PRT; 466 AA.
AC Q8JZW8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to paraneoplastic antigen MA3.
GN PMA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Strausberg R.;
RL Submitted (Aug-2002) to the ENBL/GenBank/DBJ databases.
DR ENBL; BC036726; AAH36726.1; -
DR MGD; MGI:2180565; Pma3.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008152; P:metabolism; IEA.

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DR InterPro; IPR001544; AminoTrans_IV.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 1.
DR PRINTS; PR00939; C2HCZNFINGER.
DR PROSITE; PS0158; ZF_CCHC; 1.
SQ SEQUENCE 466 AA; 54040 MW; 113787E37B0B3AAD CRC64;

Query Match 42.2%; Score 323.5; DB 11; Length 466;
Best Local Similarity 49.6%; Pred. No. 4.3e-21;
Matches 64; Conservative 38; Mismatches 26; Indels 1; Gaps 1;

QY 2 LMHIVQADNPISVVECLEAFKQVFGSLESRRTAQVRYLKPQYEGEKVSAYVLRLETL 61
Db 216 VVWVLRANNAITVKECLEALRQVFGSVDRKIAQLKCKAYQEPGKVSFVLRLETL 275

QY 62 RRAVEKRAIPRRADQVRLEQVMAGATLNQMLWCRLELKDQGGPPSPFLMLKVIREEE 121
Db 276 QKALEKNAISKNNVQTRKLKILGAILSAKLREKLKMLKQRRPPPGFLALVKLFRREEE 335

QY 122 E-EASFENE 129
Db 336 EWEATRGSE 344

RESULT 7
Q9H0A4
ID Q9H0A4 PRELIMINARY; PRT; 455 AA.
AC Q9H0A4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN DKFZP434K225.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21154917; PubMed=11230166;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansgore W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,
RA Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a Catalog of Human Genes and Proteins: Sequencing and
RT Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
RL Genome Res. 11:422-435(2001).
DR ENBL; AL136878; CAB66812.1; -
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 1.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; ZNF_C2HC; 1.
DR PROSITE; PS0158; ZF_CCHC; 1.
DR Hypothetical protein.
SQ SEQUENCE 455 AA; 51514 MW; 9AC8CC06685A8956 CRC64;

Query Match 42.2%; Score 323; DB 4; Length 455;
Best Local Similarity 52.7%; Pred. No. 4.6e-21;
Matches 68; Conservative 26; Mismatches 33; Indels 2; Gaps 1;

QY 6 VQADNPISVVECLEAFKQVFGSLESRRTAQVRYLKPQYEGEKVSAYVLRLETLRAV 65
Db 220 LRASNASITVEECLEALQVFGVPVESHKIAQVKLCKAYQAGEKVSFVLRLEPLQRAV 279

QY 66 EKRAIPRRADQVRLEQVMAGATLNQMLWCRLELKDQGGPPSPFLMLKVIREEEAS 125
Db 280 ENNVVSRNNVQTRKLKILGAILSAKLREKLKMLKQRRPPPGFLALVKLFRREEEAT 339

QY 126 F--ENESIE 132

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Db          340 LGPDRESLE 348

RESULT 8
Q9UL41      PRELIMINARY; PRT; 463 AA.
AC Q9UL41;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Paraneoplastic neuronal antigen MA3.
GN MA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gultekin S.H., Voltz R., Rosenfeld M.R., Gerstner E., Eichen J.,
RA Posner J.B., Dalmau J.;
RT "Identification of a novel cancer testis brain antigen using serum
RT antibodies from patients with testicular tumors and paraneoplastic
RT limbic encephalomyelitis.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF083116; AAF05627.1; -
DR Genew; HGNC:18742; PNMA3.
DR GO; GO:003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf_CCHC; 1.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; Znf_C2HC; 1.
DR PROSITE; PS0158; ZF_CCHC; 1.
DR SEQUENCE 463 AA; 52376 MW; 0843EF6601D8557C CRC64;

Query Match 42.2%; Score 323; DB 4; Length 463;
Best Local Similarity 52.7%; Pred. No. 4.7e-21;
Matches 68; Conservative 26; Mismatches 33; Indels 2; Gaps 1;

QY 6 VQADNPSISVEECLEAFKQVFGSLESRRTAQVRLKPYQEEGKVSAYVLRLETLRAV 65
DB 220 LRASNASITVEECLEAALQVFGVESHKIAQVKLCRAQYQAGEKVSFVLRLEPLQRAV 279

QY 66 EKRAIPRIADQVRLQVFNAGATLNQMLWCLRELKDQGPSPFLELMKVIREEEEAS 125
DB 280 ENNVSRNNVNTLKKVLSGATLPDKLRDKLKMQRKPPGFLALVKLLREEEWAT 339

QY 126 F--ENESIE 132
DB 340 LGPDRESLE 348

RESULT 9
Q8ND90      PRELIMINARY; PRT; 192 AA.
AC Q8ND90;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP434N171.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Poustka A., Wellenreuther R., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834327; CAD38995.1; -
DR KW Hypothetical protein.
FT NON_TER 1
FT SEQUENCE 192 AA; 21456 MW; 5DB17CF6A760A628 CRC64;

Query Match 38.6%; Score 295.5; DB 4; Length 192;
Best Local Similarity 46.3%; Pred. No. 5.4e-19;
Matches 62; Conservative 29; Mismatches 36; Indels 7; Gaps 2;

QY 1 DLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRLKPYQEEGKVSAYVLRLETL 60
DB 51 DVIRILKSNPAITTAECLEKALEQVFGSVESRRDAIQIKELNTYQNFGEKLSAYVIRLEPL 110
QY 61 LRRAVEKRAIPRIADQVRLQVFMAGA---TLNQMLWCLRELKDQGPSPFLELMKVI 116
DB 111 LQKWEKGAIKDNVNQARLEQVIAGANHSIAIRQLWL---TGAGEGAPNLFQLLVQI 167

QY 117 REEEEEEASFENES 130
DB 168 REEEAKEEEEEAEA 181

RESULT 10
Q95144      PRELIMINARY; PRT; 353 AA.
AC Q95144;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Paraneoplastic neuronal antigen MA1.
GN MA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RX MEDLINE=99158179; PubMed=10050892;
RA Dalmau J., Gultekin S.H., Voltz R., Hoard R., DesChamps T.,
RA Balmaceda C., Batchelor T., Gerstner E., Eichen J., Frennier J.,
RA Posner J.B., Rosenfeld M.R.;
RT "Ma1, a novel neuron- and testis-specific protein, is recognized by
RT the serum of patients with paraneoplastic neurological disorders.";
RL Brain 122:27-39 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RA Dalmau J., Rosenfeld M.R., Voltz R., Hoard R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF037364; AAD13810.3; -
DR Genew; HGNC:9158; PNMA1.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005730; C:nucleolus; TAS.
DR GO; GO:0007417; P:central nervous system development; TAS.
DR GO; GO:0007283; P:spermatogenesis; TAS.
DR SEQUENCE 353 AA; 39800 MW; 3BB41691ABE89AD3D CRC64;

Query Match 38.6%; Score 295.5; DB 4; Length 353;
Best Local Similarity 46.3%; Pred. No. 1.1e-18;
Matches 62; Conservative 29; Mismatches 36; Indels 7; Gaps 2;

QY 1 DLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRLKPYQEEGKVSAYVLRLETL 60
DB 212 DVIRILKSNPAITTAECLEKALEQVFGSVESRRDAIQIKELNTYQNFGEKLSAYVIRLEPL 271
QY 61 LRRAVEKRAIPRIADQVRLQVFMAGA---TLNQMLWCLRELKDQGPSPFLELMKVI 116
DB 272 LQKWEKGAIKDNVNQARLEQVIAGANHSIAIRQLWL---TGAGEGAPNLFQLLVQI 328

QY 117 REEEEEEASFENES 130
DB 329 REEEAKEEEEEAEA 342

RESULT 11
Q8NG07

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Query Match 37.5%; Score 287; DB 4; Length 452;
Best Local Similarity 43.8%; Pred. No. 8.4e-18;
Matches 63; Conservative 30; Mismatches 43; Indels 8; Gaps 2;
Search completed: September 27, 2004, 17:10:09
Job time : 20.7467 secs

QY 2 LMHIVQADNPISVBECEAFKQVFGSLESRRTAQVRLKPYQEEGKVSAYVLRLETL 61
DB 215 IMRVLAQNNDSITVQCILDALQIFGKEDPRASQFRFLQTSFKIGEKVSTELLRLPL 274
QY 62 BRAVEKRAIPRIADQVRLQVWAGATLNMWCLRELKQDQPPSPFLELMKVIREEE 121
DB 275 QKAVHKSPLSVRSTDMIRLKHLLARVAMTPALRGKLELLDQRCPPNFLELMKLRDEEE 334
QY 122 ---EASPENESIEPPEERDGYGR 142
DB 335 WENTAVMKNK-----EKPSGRGR 353

RESULT 15
Q9CYP2 PRELIMINARY; PRT; 353 AA.
AC Q9CYP2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 5730402C15RIK protein.
GN PNMA1 OR 5730402C15RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayaishizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK017476; BAB30762.1; -.
DR MGD; MGI:2180564; Pnmal.
SQ SEQUENCE 353 AA; 39718 MW; F7B27378B8469675 CRC64;

Query Match 37.3%; Score 285.5; DB 11; Length 353;
Best Local Similarity 47.7%; Pred. No. 8.7e-18;
Matches 63; Conservative 25; Mismatches 33; Indels 11; Gaps 3;
QY 1 DLMHIVQADNPISVBECEAFKQVFGSLESRRTAQVRLKPYQEEGKVSAYVLRLETL 60
DB 212 DVIRLKTNNAAITAECKALEQVFGSVSSSDAQVRFLNTYQNGEKLSSVIRLEPL 271
QY 61 LRRAVEKRAIPRIADQVRLQVWAGATLNMWCLRELKQDQPPSPFLELMKVIREEE 116
DB 272 LQKVDKGVIDKDNVQARLEQVIAGANHSGLRRQLWLAGAE---EGPAPNLFQLLVQI 328
QY 117 REE-----EEEA 124
DB 329 REEEAKEEEEA 340

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OM protein - protein search, using sw model

Run on: September 27, 2004, 17:04:25 ; Search time 4.86928 Seconds
(without alignments)
1593.347 Million cell updates/sec

Title: US-10-037-860-9

Perfect score: 766

Sequence: 1 DLMHIVQADNPSISVEECL.....SIEEPERDGYGRWNHEGDD 149

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	758	99.0	364	1	PMA2_HUMAN
2	741	96.7	364	1	PMA2_MACFA
3	600.5	78.4	365	1	PMA2_MOUSE
4	295.5	38.6	353	1	PMA1_HUMAN
5	294.5	38.4	353	1	PMA1_RAT
6	285.5	37.3	353	1	PMA1_MOUSE
7	274	35.8	351	1	MOPI_MACFA
8	271.5	35.4	351	1	MOPI_HUMAN
9	257.5	33.6	352	1	MOPI_MOUSE
10	102.5	13.4	554	1	NFL_BOVIN
11	98.5	12.9	525	1	NAB2_MOUSE
12	96.5	12.6	541	1	NFL_RAT
13	96	12.5	544	1	NFL_XENLA
14	95	12.4	759	1	CHLD_ARATH
15	94.5	12.3	525	1	NAB2_HUMAN
16	94	12.3	548	1	NFL_PIG
17	94	12.3	1330	1	KTNI_VULVU
18	93.5	12.2	543	1	NFL_HUMAN
19	93.5	12.2	1364	1	CND1_XENLA
20	93	12.1	399	1	RPSD_THEMA
21	91	11.9	657	1	BFS1_CHICK
22	90.5	11.8	582	1	PESC_BRARE
23	90	11.7	542	1	NFL_MOUSE
24	85	11.1	387	1	NUS4_THETH
25	83.5	10.9	631	1	RA21_HUMAN
26	83.5	10.9	776	1	TOPI_RICPR
27	83	10.8	1392	1	CND1_MOUSE
28	83	10.8	1962	1	MYS4_DROME
29	82	10.7	1225	1	SA3_HUMAN
30	82	10.7	1357	1	KTNI_HUMAN
31	81.5	10.6	105	1	RL31_AERPE
32	81.5	10.6	1898	1	TRHY_HUMAN
33	80.5	10.5	1217	1	TOPI_ZYMMO

34	80	10.4	587	1	RGP1_HUMAN
35	80	10.4	1526	1	MYS2_SCHPO
36	79.5	10.4	461	1	K6PF_THEZI
37	79	10.3	265	1	Y564_SYNY3
38	79	10.3	575	1	SP6D_BACSU
39	79	10.3	1175	1	YF19_METJA
40	78.5	10.2	339	1	YG2J_YEAST
41	78.5	10.2	436	1	RN29_HUMAN
42	78.5	10.2	1220	1	IF2P_HUMAN
43	78.5	10.2	2114	1	MY9B_MOUSE
44	78	10.2	201	1	IF3_FORGI
45	78	10.2	555	1	NFL_COTJA

ALIGNMENTS

RESULT 1

PMA2_HUMAN

ID PMA2_HUMAN STANDARD; PRT; 364 AA.

AC Q9UL42; O94959; O95145; Q9UL43;

DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Paraneoplastic antigen M2 (Onconeural antigen MA2) (Paraneoplastic neuronal antigen MM2) (40 kDa neuronal protein).

GN PMA2 OR MA2 OR KIAA0883.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RC TISSUE=Cerebellum;

RX MEDLINE=9270611; PubMed=10362822;

RA Voltz R., Gultekin S.H., Rosenfeld M.R., Gerstner E., Eichen J., Posner J.B., Dalmay J.;

RT "A serologic marker of paraneoplastic limbic and brain-stem encephalitis in patients with testicular cancer.";

RL New Engl. J. Med. 340:1788-1795(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=99156230; PubMed=10048485;

RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirotsawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

RL DNA Res. 5:355-364(1998).

RN [3]

RP IDENTIFICATION, AND SUBCELLULAR LOCATION.

RC MEDLINE=99158179; PubMed=10050892;

RA Dalmay J., Gultekin S.H., Voltz R., Hoard R., DesChamps T., Balmaceda C., Batchelor T., Gerstner E., Eichen J., Frennieri J., Posner J.B., Rosenfeld M.R.;

RT "Mal, a novel neuron- and testis-specific protein, is recognized by the serum of patients with paraneoplastic neurological disorders.";

RL Brain 122:27-39(1999).

CC -1- SUBCELLULAR LOCATION: Nuclear; nucleolar.

CC -1- TISSUE SPECIFICITY: Brain specific. In some patients suffering from cancers, it is also specifically expressed by the testicular tumor cells.

CC -1- MISCELLANEOUS: Antibodies against PMA2 are present in sera from patients suffering of paraneoplastic neurological disorders.

CC -1- SIMILARITY: Belongs to the PMA family.

CC -----

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P46060 homo sapien
Q9usi6 schizosacch
Q9hh12 thermococcu
P74557 synechocyst
P37963 bacillus su
Q58914 methanococc
P53252 saccharomyc
Q9byv6 homo sapien
O60841 homo sapien
Q9gy06 mus musculu
Q7nvq6 porphyromon
Q02916 coturnix co

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CC	EMBL; AF037365; AAD02098.1; -
DR	EMBL; AF083114; AAF05625.1; -
DR	EMBL; AF083115; AAF05626.1; -
DR	EMBL; AF286487; AAG38165.1; -
DR	EMBL; AB020690; BAA74906.1; -
DR	Genbank; HGNC:9159; PNM2.
DR	MIM; 603970; -
KW	Antigen; Tumor antigen; Nuclear protein.
FT	DOMAIN 333
FT	CONFLICT 128
FT	CONFLICT 141
FT	CONFLICT 257
FT	CONFLICT 278
FT	CONFLICT 278
SQ	SEQUENCE 364 AA; 41509 MW; 6E417AD96E3F0E93 CRC64;
Query Match 99.0%; Score 758; DB 1; Length 364;	
Best Local Similarity 99.3%; Pred. No. 9.8e-56;	
Matches 148; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 DLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRYLKPYQEGEKVSAYVLRLETL 60
DB	216 DLMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRYLKPYQEGEKVSAYVLRLETL 275
QY	61 LRRAVEKRAIPRIADQVRLQVMAGATLNQMLWCLRELKDKQGGPPSPFLMKVIREEE 120
DB	276 LRRAVEKRAIPRIADQVRLQVMAGATLNQMLWCLRELKDKQGGPPSPFLMKVIREEE 335
QY	121 EEEASFENESIEEPEERDCYGRWNHEGDD 149
DB	336 EEEASFENESIEEPEERDCYGRWNHEGDD 364
RESULT 3	
PMA2_MOUSE	
ID	PMA2_MOUSE STANDARD; PRT; 365 AA.
AC	Q8BHK0:
DT	15-MAR-2004 (Rel. 43, Created)
DT	15-MAR-2004 (Rel. 43, Last sequence update)
DT	15-MAR-2004 (Rel. 43, Last annotation update)
DE	Paraneoplastic antigen Ma2 homolog.
GN	PMA2.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Brain cortex;
RX	MEDLINE=22354683; PubMed=12466851;
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA	Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA	Shriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA	Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Gough J.,
RA	Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA	Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA	Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.B.,
RA	Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA	Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA	Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA	Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA	Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA	Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA	Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA	Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA	Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA	Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA	Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda I.,
RA	Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA	Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA	Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA	Barney E., Hayashizaki Y.;
RA	"Analysis of the mouse transcriptome based on functional annotation of
RT	60,770 full-length cDNAs."
RL	Nature 420:563-573 (2002).
CC	-I- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
CC	-I- SIMILARITY: Belongs to the PMA family.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/	
or send an email to license@isb-sib.ch).	
CC	EMBL; AB047632; BAB12156.1; -
KW	Nuclear protein.
FT	DOMAIN 333
FT	CONFLICT 364 AA; 41350 MW; 0CF72210D7EC1524 CRC64;
SQ	SEQUENCE 364 AA; 41350 MW; 0CF72210D7EC1524 CRC64;
Query Match 96.7%; Score 741; DB 1; Length 364;	

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DR EMBL; AK043718; BAC31626.1; -
DR EMBL; AK043910; BAC31700.1; -
DR MGD; MGI:2444129; Pnuma2.
KW Nuclear protein.
FT DOMAIN 333 338 POLY-GLU.
SQ SEQUENCE 365 AA; 0F90C940B9D843D9 CRC64;

Query Match 78.4%; Score 600.5; DB 1; Length 365;
Best Local Similarity 82.2%; Pred. No. 1.1e-42;
Matches 120; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

Qy 1 DLHIVQADNPISVEECLAFKQVFGSLERRTAQVRYLKPQEGEKVSAYVLRLETL 60
Db 216 DLHIVQADNPISVSGECLAFKQVFGSTERRISQVAILYKIQOEGEKISAYVLRLETL 275
Qy 61 LRRAVEKRAIPRRIADQVRLEQVNMAGATINQMLRCRLFKDQGPFPSPFLMKVIRREE 120
Db 276 LRRAVEKRAIPRRIADQVRLEQVNMAGATINQMLRCRLFKDQGPFPFLQMLKVIREEE 335
Qy 121 EEE-ASPENSIEPEERDGYGRNH 145
Db 336 EEDDAYFEQSRREPGEREGSGCWN 361

RESULT 4
PMAL_HUMAN STANDARD; PRT; 353 AA.
AC Q8ND90; O95144; Q8NG07;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Paraneoplastic antigen Mal (Neuron- and testis-specific protein 1)
DE (37 kDa neuronal protein).
DE PNMA1 OR MAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnathini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Cerebellum;
RX MEDLINE=99158179; PubMed=10050892;
RA Balmau J., Gultekin S.H., Voltz R., Hoard R., DesChamps T.,
RA Balmaceda C., Batchelor T., Gersner E., Eichen J., Fremier J.,
RA Posner J.B., Rosenfeld M.R.;
RT "Mal, a novel neuron- and testis-specific protein, is recognized by
RT the serum of patients with paraneoplastic neurological disorders."
RL Brain 122:27-39(1999).
[2]
SEQUENCE FROM N.A.
RP Schueller M.M., Jenne D.E., Schutze dit Belkner N., Hohlfield R.,
RA Voltz R.;
RT "Mal (PNMA1).";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RP TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 162-353 FROM N.A.
RC TISSUE=Testis;
RA Poustka A., Wellenreuther R., Mewes H.-W., Weill B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar. In tumor cells, it is
CC cytoplasmic.
CC -!- TISSUE SPECIFICITY: Testis and brain specific. In some patients
CC suffering from cancers, it is also specifically expressed by the
CC paraneoplastic tumor cells.
CC -!- MISCELLANEOUS: Antibodies against PNMA1 are present in sera from
CC patients suffering of paraneoplastic neurological disorders.
CC -!- SIMILARITY: Belongs to the PNMA family.
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DR EMBL; AF037364; AAD13810.3; -
DR EMBL; AF320308; AAN05100.1; -
DR EMBL; BC039577; AAH39577.1; -
DR EMBL; AL834327; CAD38995.1; -
DR GeneW; HGNC:9158; PNMA1.
DR MIM; 604010; -
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005730; C:nucleolus; TAS.
DR GO; GO:0007417; P:central nervous system development; TAS.
DR GO; GO:0007283; P:spermatogenesis; TAS.
KW Antigen; Tumor antigen; Nuclear protein.
FT DOMAIN 335 341 POLY-GLU.
SQ SEQUENCE 353 AA; 8B7F5B5AEDA25961 CRC64;

Query Match 38.6%; Score 295.5; DB 1; Length 353;
Best Local Similarity 46.3%; Pred. No. 1.9e-17;
Matches 62; Conservative 29; Mismatches 36; Indels 7; Gaps 2;

Qy 1 DLHIVQADNPISVEECLAFKQVFGSLERRTAQVRYLKPQEGEKVSAYVLRLETL 60
Db 212 DVIRILKSNPFAITAECLKALEQVFGSVESRDQIKFLNTYQNPGEKLSAYVLRLEPL 271
Qy 61 LRRAVEKRAIPRRIADQVRLEQVWAGA-----TLNQMLWCLRELKQDGPFPFLMKVI 116
Db 272 LQKVVEKGAIDKDNVNOARLEQVIAGNHSGAIRRLWL---TGAGEGPAPNLFQLLVQI 328
Qy 117 REEEEREASFENES 130
Db 329 REEEAKEEEEA 342

RESULT 5
PMAL_RAT STANDARD; PRT; 353 AA.
AC Q8VHZ4;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Paraneoplastic antigen Mal homolog.
GN PNMA1 OR MAL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RP

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RX MEDLINE=99158179; PubMed=10050892;
RA Dalmau J., Gultekin S.H., Voltz R., Hoard R., DesChamps T.,
RA Balmaceda C., Batchelor T.B., Gerstner E., Eichen J., Frennier J.,
RA Posner J.B., Rosenfeld M.R.;
RT "Maf, a novel neuron- and testis-specific protein, is recognized by
RT the serum of patients with paraneoplastic neurological disorders.";
RL Brain 122:27-39(1999).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
CC -!- TISSUE SPECIFICITY: Testis and brain specific.
CC -!- SIMILARITY: Belongs to the PNUA family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF335505; AAL73196.1; -.
KW Nuclear protein.
FT DOMAIN 335 341 POLY-GLU.
SQ SEQUENCE 353 AA; 39793 MW; PFC3A717FDCEDA3 CRC64;

Query Match 38.4%; Score 294.5; DB 1; Length 353;
Best Local Similarity 47.0%; Pred. No. 2.3e-17;
Matches 63; Conservative 27; Mismatches 37; Indels 7; Gaps 2;

QY 1 DLMHIVQADNPSTISVEECLEAFKQVFGSLESRTAQVRYLKPYQEGEKVSAYVLRLETL 60
Db 212 DVIRILKTNPAITTAECLEKALEQVFGSVESRDQVRFINTYQNGEKLSSVIRLEPL 271

QY 61 LRRAVEKRAIPRIADQVRLQVLMAGA-----TINQMLWCLRELKQDQPPSPFLELMKVI 116
Db 272 LQKVVDKGVIDKNVQNRLEQVIAGANHSGLRRQLWL---TGATEGPAPNLFQLLVQI 328

QY 117 REEEEEEAFENES 130
Db 329 REEEAKEEEEAFA 342

RESULT 6
PMAL_MOUSE
ID PMAL_MOUSE STANDARD; PRT; 353 AA.
AC Q8C1C8; Q9CVP2;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Paraneoplastic antigen Maf homolog.
GN PMAL OR MAF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Brain, and Embryo;
MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimonod S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Naglath D.R., Numaiz L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Nakata K., Okido T., Pavan W.J., Ferte G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

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RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Yanagisawa M., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
CC -!- SIMILARITY: Belongs to the PNUA family.
CC
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CC
CC EMBL; AK017476; BAB30762.1; -.
DR EMBL; AK028331; BAC25885.1; -.
DR MGD; MGI:2180564; Pnmal.
KW Nuclear protein.
FT DOMAIN 336 341 POLY-GLU.
FT CONFLICT 136 136 T -> M (IN REF. 1; BAB30762).
SQ SEQUENCE 353 AA; 39688 MW; 18CEDC3AC4E70939 CRC64;

Query Match 37.3%; Score 285.5; DB 1; Length 353;
Best Local Similarity 47.7%; Pred. No. 1.3e-16;
Matches 63; Conservative 25; Mismatches 33; Indels 11; Gaps 3;

QY 1 DLMHIVQADNPSTISVEECLEAFKQVFGSLESRTAQVRYLKPYQEGEKVSAYVLRLETL 60
Db 212 DVIRILKTNPAITTAECLEKALEQVFGSVESRDQVRFINTYQNGEKLSSVIRLEPL 271

QY 61 LRRAVEKRAIPRIADQVRLQVLMAGA-----TINQMLWCLRELKQDQPPSPFLELMKVI 116
Db 272 LQKVVDKGVIDKNVQNRLEQVIAGANHSGLRRQLWLAGE---EGEAPNLFQLLVQI 328

QY 117 REE-----EEEA 124
Db 329 REEEAKEEEEA 340

RESULT 7
MOP1_MACFA
ID MOP1_MACFA STANDARD; PRT; 351 AA.
AC Q95KI4;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Modulator of apoptosis 1 (MAP-1).
GN MOAP1.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
[1]
SEQUENCE FROM N.A.
TISSUE=Temporal cortex;
RA Oseada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain CDNA
RT libraries.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Mediates caspase-dependent apoptosis (By similarity).

```



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QY 118 E---EEEEA 124
Db 331 DYEAEEEEE 340

RESULT 9
ID MOP1 MOUSE STANDARD; PRT; 352 AA.
AC Q9E9H6;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Modulator of apoptosis 1 (MAP-1).
GN MOAP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21264738; PubMed=11060313;
RA Tan K.O., Tan K.M.L., Chan S.-L., Yee K.S.Y., Bevoit M., Ang K.C.,
RA Yu V.C.;
RT "MAP-1, a novel proapoptotic protein containing a BH3-like motif that
RT associates with Bax through its Bcl-2 homology domains.";
RL J. Biol. Chem. 276:2802-2807(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=1217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez J., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic, and Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smaluk D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

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RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -|- FUNCTION: Mediates caspase-dependent apoptosis.
CC -|- SUBUNIT: Homodimer. Binds BAX, BCL2 and BCLX (By similarity).
CC -|- DOMAIN: The BH3-like domain is required for association with BAX
CC and for mediating apoptosis. The three BH domains (BH1, BH2, and
CC BH3) of BAX are all required for mediating protein-protein
CC interaction (By similarity).
CC -|- SIMILARITY: Belongs to the PNMA family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC entities requires a license agreement. (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF305551; AAG31787.1; -
CC EMBL; AK019599; BAB31810.1; -
CC EMBL; BC014715; AAH14715.1; -
CC EMBL; BC055374; AAH55374.1; -
CC MGD; MGI:191555; Moap1.
KW Apoptosis.
FT SITE 120 127 BH3-LIKE.
FT DOMAIN 335 340 POLY-GLU.
FT CONFLICT 57 57 R -> K (IN REF. 3; AAH55374).
SQ SEQUENCE 352 AA; 39404 MW; 8F4630D080495D98 CRC64;

Query Match 33.6%; Score 257.5; DB 1; Length 352;
Best Local Similarity 38.6%; Pred. No. 2.7e-14;
Matches 54; Conservative 35; Mismatches 44; Indels 7; Gaps 2;

QY 1 DLMHIVQADNPISVVEECLEAFKQVFGSLESRTAQVRLKPVQEGEKVSAVLRLETL 60
Db 218 EIIRVLKINNPFITVAECUKLTETIPGIIDNRAIQVRYLTYYQKTDKLSAVLRLEPL 277
QY 61 LRRRAVEKRAIPRIADQVRLQVMAQATLQMLWCRLKQDQPPPSFLELMKVIREEE 120
Db 278 LQKLQVKGALKEVNVQARLDQVIAGAVHKSVR--RELGLPEGSPAPGLQLLTLLDKKE 335
QY 121 EEEAFENESIPEPERDGY 140
Db 336 AEE-----EVLVLALEGY 350

RESULT 10
NFL_BOVIN STANDARD; PRT; 554 AA.
AC P02548; P79127;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurofilament triplet L protein (68 kDa neurofilament protein)
DE (Neurofilament light polypeptide) (NF-L) (Micro glutamic acid-rich
DE protein).
GN NEFL.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Holstein; TISSUE=Brain;
RA Hill W.D., Zhang L., Balin B.J., Sprinkle T.J.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 468-554.
RX MEDLINE=85154567; PubMed=3884373;
RA Isobe T., Okuyama T.;
RT "Brain micro glutamic acid-rich protein is the C-terminal endpiece of
RT the neurofilament 68-kDa protein as determined by the primary

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RT sequence.";
RL FEBS Lett. 182:389-392(1985).
CC -!- FUNCTION: Neurofilaments usually contain three intermediate
CC filament proteins: L, M, and H which are involved in the
CC maintenance of neuronal caliber.
CC -!- DOMAIN: THE EXTRA MASS AND HIGH CHARGE DENSITY THAT DISTINGUISH
CC THE NEUROFILAMENT PROTEINS FROM ALL OTHER INTERMEDIATE FILAMENT
CC PROTEINS ARE DUE TO THE TAILPIECE EXTENSIONS. THIS REGION MAY FORM
CC A CHARGED SCAFFOLDING STRUCTURE SUITABLE FOR INTERACTION WITH
CC OTHER NEURONAL COMPONENTS OR IONS.
CC -!- MISCELLANEOUS: NF-L IS THE MOST ABUNDANT OF THE THREE
CC NEUROFILAMENT PROTEINS AND, AS THE OTHER NONEPITHELIAL
CC INTERMEDIATE FILAMENT PROTEINS, IT CAN FORM HOMOPOLYMERIC 10-NM
CC FILAMENTS.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U83919; AAB41543.1; -.
CC InterPro; IPR006821; Filament_head.
CC InterPro; IPR001664; IF.
CC Pfam; PF00038; filament; 1.
CC Pfam; PF04732; filament_head; 1.
CC PROSITE; PS00226; IF; 1.
CC Intermediate filament; Coiled coil; Neuron.
CC INIT_MET 0 0
CC DOMAIN 1 92
CC DOMAIN 93 396
CC DOMAIN 397 554
CC DOMAIN 554 124
CC DOMAIN 125 137
CC DOMAIN 138 233
CC DOMAIN 234 252
CC DOMAIN 253 271
CC DOMAIN 272 280
CC DOMAIN 281 396
CC DOMAIN 397 443
CC DOMAIN 444 554
CC DOMAIN 554 500
CC CONFLICT 494 500
CC CONFLICT 509 509
CC CONFLICT 509 509
CC SEQUENCE 554 AA; 62514 MW; D772B81CA2C31CIA CRC64;
CC -----
Query Match
Best Local Similarity 13.4%; Score 102.5; DB 1; Length 554;
Matches 41; Conservative 24; Mismatches 66; Indels 47; Gaps 6;
Qy 2 LMHIVQADNPISIVVECLAFKQVFGSLRSRTAQVRLKPYQE----- 45
Db 333 LQELLEDKQADISAMQ--DTINKLENLRTTKSEMARYLKEYQDLLNVKMDLIEIAAYR 390
Qy 46 ---EGEK-----VSAYVLRLETLRRA-----VEKRAIPRIADQVRL 81
Db 391 KLEGEETRLSFTSGVSLTTGTQSSQVFGSAYGGLQTSSYLSARSFSPSYTSHVQEE 450
Qy 82 QVMAGATLNQMLCRRLKQDQPPSPFLELMKVIREEEBEAEAFENESIEPEPERDG 139
Db 451 QIEVEETIEA---AKAEAEKDE--PPSEGEAEKEKEAEAEAEAEAEAEAE 503
RESULT 11
NAB2 MOUSE
ID NAB2 MOUSE STANDARD; PRT; 525 AA.
AC Q61127;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE NGFI-A binding protein 2 (EGR-1 binding protein 2).

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GN NAB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=96251303; PubMed=8668170;
RA Svaren J., Sevetson B.R., Apel E.D., Zimonjic D.B., Popescu N.C.,
RA Milbrandt J.;
RT "NAB2, a corepressor of NGFI-A (Egr-1) and Krox20, is induced by
RT proliferative and differentiative stimuli.";
RL Mol. Cell. Biol. 16:3545-3553(1996).
[2]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=97271553; PubMed=9126479;
RA Svaren J., Apel E.D., Simburger K.S., Jenkins N.A., Gilbert D.J.,
RA Copeland N.A., Milbrandt J.;
RT "The Nab2 and Stat6 genes share a common transcription termination
RT region.";
RL Genomics 41:33-39(1997).
CC -!- FUNCTION: Acts as a transcriptional repressor for zinc finger
CC transcription factors EGR1 and EGR2. Isoform 2 lacks repression
CC ability.
CC -!- SUBUNIT: Homomultimeric may associate with EGR1 bound to DNA (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: NUCLEAR. ISOFORM 2 IS NOT LOCALIZED TO THE
CC NUCLEUS.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q61127-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q61127-2; Sequence=VSP_003388, VSP_003389;
CC -!- TISSUE SPECIFICITY: Highly expressed in brain and thymus, and at
CC lower levels in spleen, kidney, heart and testis. Isoform 1 is
CC predominantly expressed in testis, whereas isoform 3 is more
CC abundant in thymus.
CC -!- INDUCTION: By serum stimulation.
CC -!- DOMAIN: The NAB conserved domain 1 (NCD1) interacts with EGR1
CC inhibitory domain and mediates multimerization.
CC -!- DOMAIN: The NAB conserved domain 2 (NCD2) is necessary for
CC transcriptional repression.
CC -!- SIMILARITY: BELONGS TO THE NAB FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U47543; AAC52650.1; -.
CC MGD; MGI:107563; Nab2.
CC InterPro; IPR006989; Nab_cent.
CC InterPro; IPR006988; Nab_N.
CC Pfam; PF04904; NCD1; 1.
CC Pfam; PF04905; NCD2; 1.
CC Transcription regulation; Repressor; Alternative splicing.
CC DOMAIN 35 113 NCD1.
CC DOMAIN 267 356 NCD2.
CC DOMAIN 353 384
CC VARSPLIC 320 322 LTI -> ASL (in isoform 2).
CC VARSPLIC 323 525 /FTId=VSP_003388.
CC VARSPLIC 323 525 Missing (in isoform 2).
CC VARSPLIC 323 525 /FTId=VSP_003389.
CC SEQUENCE 525 AA; 56653 MW; FED428E9A8BD804 CRC64;
Query Match
Best Local Similarity 12.9%; Score 98.5; DB 1; Length 525;

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10-OCT-2003 (Rel. 42, Last annotation update)
 Neurofilament triplet L protein (Neurofilament light polypeptide) (NP-L).
 Xenopus laevis (African clawed frog).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92356194; PubMed=1494944;
 RA Charnas L.R., Szaro B.G., Gainer H.;
 RT "Identification and developmental expression of a novel low molecular weight neuronal intermediate filament protein expressed in Xenopus laevis.";
 RL J. Neurosci. 12:3010-3024(1992).
 CC -!- FUNCTION: Neurofilaments usually contain three intermediate filament proteins: L, M, and H which are involved in the maintenance of neuronal caliber.
 CC -!- MISCELLANEOUS: NP-L IS THE MOST ABUNDANT OF THE THREE NEUROFILAMENT PROTEINS AND, AS THE OTHER NONEPITHELIAL INTERMEDIATE FILAMENT PROTEINS, IT CAN FORM HOMOPOLYMERIC 10-NM FILAMENTS.
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC EMBL; M86654; AA83018.1; -;
 DR InterPro; IPR006821; Filament_head.
 DR InterPro; IPR001664; IF.
 DR Pfam; PF00038; filament; 1.
 DR Pfam; PF04732; filament_head; 1.
 DR PROSITE; PS00226; IF; 1.
 KW Intermediate filament; Coiled coil; Neurone.
 FT DOMAIN 1 87 HEAD.
 FT DOMAIN 88 390 ROD.
 FT DOMAIN 391 544 TAIL.
 FT DOMAIN 88 119 COIL 1A.
 FT DOMAIN 120 132 COIL 1B.
 FT DOMAIN 133 228 COIL 1C.
 FT DOMAIN 229 246 COIL 2A.
 FT DOMAIN 247 265 COIL 2B.
 FT DOMAIN 266 274 COIL 2C.
 FT DOMAIN 275 390 TAIL, SUBDOMAIN A.
 FT DOMAIN 391 435 TAIL, SUBDOMAIN B (ACIDIC).
 FT DOMAIN 436 544 TAIL, SUBDOMAIN B (ACIDIC).
 FT DOMAIN 441 538 GLU-RICH.
 FT DOMAIN 464 469 POLY-GLU.
 SQ SEQUENCE 544 AA; 61861 MW; 76D911B896E97201 CRC64;
 Query Match 12.5%; Score 96; DB 1; Length 544;
 Best Local Similarity 23.0%; Pred. No. 1;
 Matches 42; Conservative 19; Mismatches 56; Indels 66; Gaps 6;
 9 DNPISVEECLEAFQVFGSLESRTAQVRLKPYQE-----RGEK 49
 332 DKQGEIAGQMDINKLEELRLTSEMAVRLKQYDQLLNVKMLDIEIAYRKLLEGEE 391
 50 V-----SAYVRLTLLRAVEKRAIPRIADQVRLQVWAG 86
 392 TRLSFGVGALTSGYTQSAPVFGSAYSLQSSVM---TSRAPTYTSHVQEQDIE 447
 87 ATLQMLWCLRLREUKDQPPSPFLMKVIREEEEPASFENESIEEPERDGYGRWNH 146
 448 ETIES---SRAEAKAEAP-----EEEEEAEEEGEGGEAEE-----GEE 487

QY 147 GDD 149
 DB 488 GEE 490
 RESULT 14
 CHLD_ARATH
 ID CHLD_ARATH STANDARD; PRT; 759 AA.
 AC Q9SJE1; Q9SW5;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Magnesium-chelatase subunit chld, chloroplast precursor (Mg-protoporphyrin IX chelatase) (Mg-chelatase subunit D).
 GN CHLD OR ATIG08520 OR T27G7.20.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 SEQUENCE FROM N.A.
 RP STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K., Dunn P., Egtu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y., Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., Kim C.J., Koo H.B., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A., Militischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana";
 RT Nature 408:816-820(2000).
 RL [2]
 SEQUENCE OF 32-759 FROM N.A.
 RP STRAIN=cv. C24;
 RC Green J., Jensen P.E., Gibson L.C.D., Hunter C.N.;
 RA "Characterization of the magnesium protoporphyrin chelatase chld subunit from Arabidopsis thaliana cv. C24";
 RT Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RL -!- FUNCTION: Involved in chlorophyll biosynthesis; introduces a magnesium ion into protoporphyrin IX to yield Mg-protoporphyrin IX.
 CC -!- PATHWAY: Chlorophyll biosynthesis.
 CC -!- SUBCELLULAR LOCATION: Chloroplast stroma.
 CC -!- SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNITS D/I FAMILY.
 CC -!- SIMILARITY: Contains 1 VFMA domain.
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to erroneous gene model prediction.
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 CC EMBL; AC006932; AAF22895.1; ALT_SEQ.
 DR EMBL; AF083555; AAD52031.1; -;
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR000523; Mg_chelatase_chII.
 DR InterPro; IPR002035; VWF_A.

DR Pfam: PR01078; Mg chelatase; 1.
 DR SMART; SM00382; AXA; 1.
 DR SMART; SM00327; VWA; 1.
 DR PROSITE; PS0234; VWA; 1.
 KW Photosynthesis; Chlorophyll biosynthesis; ATP-binding; Chloroplast;
 KW Transit peptide.
 FT TRANSIT 1 ?
 FT CHAIN 1 ?
 FT DOMAIN 557 759
 FT DOMAIN 411 418
 FT DOMAIN 425 438
 FT CONFLICT 70 70
 FT CONFLICT 150 150
 FT CONFLICT 270 270
 FT CONFLICT 285 286
 FT CONFLICT 314 314
 FT CONFLICT 379 379
 FT CONFLICT 426 426
 FT CONFLICT 426 426
 SQ SEQUENCE 759 AA; 83154 MW; A4169319E1247BD1 CRC64;

Query Match 12.4%; Score 95; DB 1; Length 759;
 Best Local Similarity 24.0%; Pred. No. 1.8;
 Matches 40; Conservative 21; Mismatches 42; Indels 64; Gaps 6;

QY 16 ECLAEAFKQVFGSLERTRAQV---RYLKPQY-----EEGKVSAYVL 55
 Db 307 ERCNEVFRWNEBETAKTQILAREYLKDVKISREQLKYLVEAVRGVGGVGHRAELYAA 366
 QY 56 RLETL-----LRRAVEKRAIPRIADQVRLEQVQVAGATNQLMCRLEIK 101
 Db 367 RVAKCLAAEGREKVTIDLRKAVELVILPRSLDETPEQ-----Q 408
 QY 102 DQGGPP-----SLELMKVIREEESEAFENESIE-----PRE 136
 Db 409 NOPPPPPPPQNSGESENEEQEEDSENEENEOQQDQIPPE 455

RESULT 15
 ID NAB2_HUMAN STANDARD; PRT; 525 AA.
 AC Q15742; Q76006; Q14797;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE NGFI-A binding protein 2 (EGR-1 binding protein 2) (Melanoma-associated delayed early response protein) (MADER protein).
 DE NAB2 OR MADER.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Placenta;
 RX MEDLINE=96251303; PubMed=8668170;
 RA Svarén J., Severson B.R., Apel E.D., Zimonjic D.B., Popescu N.C., Milbrandt J.;
 RA "NAB2, a corepressor of NGFI-A (Egr-1) and Krox20, is induced by proliferative and differentiative stimuli.";
 RT Mol. Cell. Biol. 16:3545-3553(1996).
 RN [2]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RA Gerlinger M., Johnson J.P.;
 RT "Genomic organization of the Mader/NAB2 gene";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE OF 50-525 FROM N.A. (ISOFORM 1).
 RX MEDLINE=96243039; PubMed=8649813;
 RA Kirsch K.H., Korradi V., Johnson J.P.;
 RT "Mader: a novel nuclear protein over expressed in human melanomas.";
 RN Oncogene 12:963-971(1996).
 RN [4]
 RN PARTIAL SEQUENCE FROM N.A. (ISOFORM 3).
 RP

Johnson J.P.;
 Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 [5]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=97271553; PubMed=9126479;
 RA Svarén J., Apel E.D., Simburger K.S., Jenkins N.A., Gilbert D.J., Copeland N.A., Milbrandt J.;
 RA "The NAB2 and Stat6 genes share a common transcription termination region";
 RT Genomics 41:33-39(1997).
 RL
 CC -!- FUNCTION: Acts as a transcriptional repressor for zinc finger transcription factors EGR1 and EGR2. Isoform 2 lacks repression ability (By similarity).
 CC -!- SUBUNIT: Homomultimers may associate with EGR1 bound to DNA (By similarity).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR. ISOFORM 2 IS NOT LOCALIZED TO THE NUCLEUS (BY SIMILARITY).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q15742-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q15742-2; Sequence=VSP_003385, VSP_003386;
 CC Name=3;
 CC IsoId=Q15742-3; Sequence=VSP_003387;
 CC TISSUE SPECIFICITY: Widely expressed at low levels. Highly expressed in melanoma cell lines.
 CC -!- INDUCTION: By serum and PMA stimulation.
 CC -!- DOMAIN: The NAB conserved domain 1 (NCD1) interacts with EGR1 inhibitory domain and mediates multimerization.
 CC -!- DOMAIN: The NAB conserved domain 2 (NCD2) is necessary for transcriptional repression.
 CC -!- SIMILARITY: BELONGS TO THE NAB FAMILY.
 CC
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 CC
 CC EMBL; U48361; AAC50589.1; -;
 DR EMBL; AF268380; AAF72545.1; -;
 DR EMBL; X70991; CAA50318.1; -;
 DR EMBL; AJ011081; CAA09472.1; -;
 DR Genew; HGNC:7627; NAB2.
 DR MIM; 602381; -;
 DR GO; GO:0003714; F:transcription co-repressor activity; TAS.
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR GO; GO:0007399; P:neurogenesis; TAS.
 DR InterPro; IPR006989; Nab_cent.
 DR InterPro; IPR006988; Nab_N.
 DR Pfam; PF04904; NCD1; 1.
 DR Pfam; PF04905; NCD2; 1.
 DR Transcription regulation; Repressor; Alternative splicing.
 FT DOMAIN 35 113 NCD1.
 FT DOMAIN 267 356 NCD2.
 FT DOMAIN 353 384
 FT VARSPLIC 320 322
 FT LTI -> ASP (in isoform 2).
 FT VARSPLIC 323 525
 FT VARSPLIC 426 489
 FT VARSPLIC 257 258
 FT CONFLICT 525 AA; 56594 MW; 38CF6CFE73756F9 CRC64;
 SQ SEQUENCE

Query Match 12.3%; Score 94.5; DB 1; Length 525;
 Best Local Similarity 23.5%; Pred. No. 1.3;
 Matches 36; Conservative 29; Mismatches 53; Indels 35; Gaps 5;

```
Qy      4  HUVQADNPSISVEECLEAFKQVFGSLERRTAQVRYLKPYOEGEKUS-----A 52
Db      280 HIFEMDDNDSQKEEIRKYSIIYGRFDSKR-----REGQLSLHSLTINEAAQ 328
Qy      53  YVLRLETLRRRAVEKRAIPRIADQVRLEQVMAGATLN--OMLWCRRLRELKD----- 102
Db      329 FCMDNTILLRRVELFSLSRQVARESTYLSLKGSRLLHPBELGGPPLKKLKQEVGEQSHP 388
Qy      103 --QGPPPSFLELMKVIREE-EEEAASFENESIE 132
Db      389 EIQOPPPGPESYVPPYRPSLEDSASLSGESLD 421
```

Search completed: September 27, 2004, 17:08:45
Job time : 6.86928 secs

B/ANK

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 27, 2004, 17:05:46 ; Search time 6.57353 Seconds
(without alignments)
2180.341 Million cell updates/sec

Title: US-10-037-860-9

Perfect score: 766

Sequence: 1 DLMHVQADNPSISVEECLE.....SIEEPEDRGYGRWNHGGDD 149

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 28366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 28366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102.5	13.4	554	2 JMW0094	neurofilament prot
2	96	12.5	544	2 B44841	low molecular weig
3	94.5	12.3	475	2 S31927	drop9 protein - hu
4	94	12.3	548	1 QPPGL	neurofilament trip
5	93.5	12.2	544	2 S07144	neurofilament trip
6	93.5	12.2	1364	2 T14900	condensin XCAP-D2
7	93	12.1	399	2 G72253	RNA polymerase sig
8	91	11.9	657	2 S32739	filensin - chicken
9	90	11.7	543	1 QPMSL	neurofilament trip
10	90	11.7	592	2 JC7709	testis-specific ki
11	89.5	11.7	800	2 T00034	SART-1 protein - h
12	86.5	11.3	778	2 B86218	protein T27G7.20 [
13	85	11.1	387	1 S52274	transcription term
14	85	11.1	800	2 T19627	hypothetical prote
15	84.5	11.0	234	2 F70416	hypothetical prote
16	84.5	11.0	1184	2 T41515	coiled coil protei
17	84.5	11.0	1300	2 I53799	CGI protein - huma
18	84	11.0	315	2 T26186	hypothetical prote
19	83.5	10.9	776	2 H71698	DNA topoisomerase
20	83	10.8	1175	2 C35815	myosin heavy chain
21	83	10.8	1175	2 D35815	myosin heavy chain
22	83	10.8	1201	2 A35815	myosin heavy chain
23	83	10.8	1201	2 B35815	myosin heavy chain
24	83	10.8	2385	2 A32491	myosin heavy chain
25	83	10.8	2411	2 B32491	myosin heavy chain
26	82	10.7	576	2 AE3491	SSU ribosomal prot
27	82	10.7	1356	2 S32763	kinectin 1 - human
28	81.5	10.6	105	2 H72708	probable ribosomal
29	81.5	10.6	425	2 S76760	transcription init

ALIGNMENTS

RESULT 1

JW0094

neurofilament protein-L - bovine

N:Alternate names: NF-L

C:Species: Bos primigenius taurus (cattle)

C>Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999

C:Accession: JW0094

R:Hashimoto, R.; Nakamura, Y.; Goto, H.; Wada, Y.; Sakoda, S.; Kaibuchi, K.; Inagaki, M.

Biochem. Biophys. Res. Commun. 245, 407-411, 1998

A:Title: Domain- and site-specific phosphorylation of bovine NF-L by Rho-associated kina

A:Reference number: JW0094; MUID:98238650; PMID:9571164

A:Accession: JW0094

A:Molecule type: protein

A:Residues: 1-554 <HAS>

C:Comment: Domain- and site-specific phosphorylation by Rho-kinase regulates the assembl

C:Superfamily: cytoskeletal keratin

Query Match 13.4%; Score 102.5; DB 2; Length 554;

Best Local Similarity 23.0%; Pred. No. 0.46;

Matches 41; Conservative 24; Mismatches 66; Indels 47; Gaps 6;

QY 2 LMHVQADNPSISVEECLEAFKQVFGSLRSRTAQVRLKPYQE----- 45

Db 333 LQLEDKQNDISAMQ--DTINKLEBLRTTKSEMARYLKEYQDLLNYKMALDIEIAAYR 390

QY 46 ---EGEK-----VSAYVLRLETLRRA-----VEKRAIPRIADQVPLE 81

Db 391 KLEGEETRLSFTSVGSLTTGTTQSSQVFGRSAYGGLQTSYLSMSARSFPYSYTSHVQEE 450

QY 82 QVMAGATINQMLWCRLKELKQDQPPSPFLELMKVIREEEEEEAEAFENESIEEPEERDG 139

Db 451 QIEVEETIEA--AKAEAEKDE--PPSEGEAEKEKEKEAEAEAEAEAEAEAE 503

RESULT 2

B44841

low molecular weight neurofilament protein XNF-L - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995

C:Accession: B44841

R:Charnas, L.R.; Szaro, B.G.; Gainer, H.

J. Neurosci. 12, 3010-3024, 1992

A:Title: Identification and developmental expression of a novel low molecular weight neu

A:Reference number: A44841; MUID:92356194; PMID:1494944

A:Accession: B44841

A:Molecule type: mRNA

A:Residues: 1-544 <CHA>

A:Experimental source: brain

A:Note: sequence inconsistent with the nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIN:110225, NCBI:110226)

C:Superfamily: cytoskeletal keratin

Query Match 12.5%; Score 96; DB 2; Length 544;
Best Local Similarity 23.0%; Pred. No. 1.6;
Matches 42; Conservative 19; Mismatches 56; Indels 66; Gaps 6;
QY 9 DNPSISVVECLAFKQVFGSLERRTAQVRLKPYOE-----EGEK 49
DB 332 DKQGEIAGQDAINKLEELRTKSEMARYLKEYQDLLNVKVALDIEIAAYRKLEEGE 391
QY 50 V-----SAYVLRLETLRRRAVEKRAIPRRRIADQVRLQVWAG 86
DB 332 TRLFSGVCAITSGYTQAPVGRGAYSLOSSYM-----TSRAFFYYSSHVQEEQLDIE 447
QY 87 AFLNQMLWCRLELKDQPPSPFLMLKVIREEEAEAFENESIEPPEPDYGRWNHE 146
DB 448 ETIES---SRAEAKAEAF-----EEEEAEAEEGEGEAEAE-----GEE 487
QY 147 GPD 149
DB 488 GEE 490

RESULT 3

S31927
drop9 protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Sep-1997
C:Accession: S31927
R:Kirsch, K.
Submitted to the EMBL Data Library, February 1993
A:Reference number: S31927
A:Accession: S31927
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-475 <KIR>
A:Cross-references: EMBL:X70991; NID:G38459; PID:G38460

Query Match 12.3%; Score 94.5; DB 2; Length 475;
Best Local Similarity 23.5%; Pred. No. 1.8;
Matches 36; Conservative 29; Mismatches 53; Indels 35; Gaps 5;
QY 4 HIVQADNPISIVVECLAFKQVFGSLERRTAQVRLKPYOEKEKVS-----A 52
DB 230 HIFEMDNDQKEETIRKYIIIGRFDKR-----REGKQLSLHELINAEAAQ 278
QY 53 YVLRLETLRRRAVEKRAIPRRRIADQVRLQVWAGATLN--OMLWCRLELKD----- 102
DB 279 FCMRDNTLLRRVELFSLRSQVARESTYLSLKGSLRHLPEELGPPPLKILKQEVGQSHP 338
QY 103 --QGPSPFLMLKVIREE-EEAEAFENESIE 132
DB 339 EIQQPPPGPESYVPPYRPSLEEDSASLSGSLD 371

RESULT 4

QFPC L
neurofilament triplet L protein - pig
N:Alternate names: 68k neurofilament protein
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 15-Nov-1984 #sequence_revision 28-May-1986 #text_change 10-Oct-1997
C:Accession: A91337; A90973; A34569; A02963
R:Geisler, N.; Plessmann, U.; Weber, K.
FEBS Lett. 182, 475-478, 1985
A:Title: The complete amino acid sequence of the major mammalian neurofilament protein
A:Reference number: A91337; MUID:85154583; PMID:3920075
A:Accession: A91337
A:Molecule type: protein
A:Residues: 1-547 <GB1>
R:Geisler, N.; Kaufmann, E.; Fischer, S.; Plessmann, U.; Weber, K.
EMBO J. 2, 1295-1302, 1983
A:Title: Neurofilament architecture combines structural principles of intermediate filaments
A:Reference number: A90973
A:Accession: A90973

A:Molecule type: protein
A:Residues: 1-82; 278-548 <GE2>
A>Note: residue 322 is either lysine or arginine
R:Gonda, Y.; Nishizawa, K.; Ando, S.; Kitamura, S.; Minoura, Y.; Nishi, Y.; Inagaki, M.
Biochem. Biophys. Res. Commun. 167, 1316-1325, 1990
A:Title: Involvement of protein kinase C in the regulation of assembly-disassembly of ne
A:Reference number: A34569; MUID:90211318; PMID:2108674
A:Accession: A34569
A:Status: preliminary
A:Molecule type: protein
A:Residues: 9-14; 23-29; 30-53 <GON>
C:Comment: Mammalian neurofilaments usually contain three polypeptides, L, M, and H (wit
ke all other intermediate filament proteins: a conserved alpha-helical region, whose hel
C:Comment: The amino-terminal headpiece is basic with a high content of hydroxyamino aci
al beta turns; domain b is acidic and rich in glutamic acid and lysine residues.
C:Comment: The extra mass and high charge density that distinguish the neurofilament pro
charged scaffolding structure suitable for interaction with other neuronal components o
C:Comment: The boundaries of the domains between residues 70-92 and 399-402 are not yet
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:1-70/Domain: head <HED>
F:92-123/Domain: coil 1a, alpha-helical rod <R1A>
F:137-232/Domain: coil 1b, alpha-helical rod <R1B>
F:255-399/Domain: coil 2, alpha-helical rod <RD2>
F:402-548/Domain: tail <TAI>
F:402-442/Region: tail subdomain a
F:443-548/Region: tail subdomain b

Query Match 12.3%; Score 94; DB 1; Length 548;
Best Local Similarity 22.0%; Pred. No. 2.4;
Matches 44; Conservative 24; Mismatches 70; Indels 62; Gaps 7;
QY 2 LMHIVQADNPISIVVECLAFKQVFGSLERRTAQVRLKPYOE----- 45
DB 332 LOELDKQADISAMQ--DTINKLENELRTTSEMARYLKEYQDLLNVKVALDIEIAAYR 389
QY 46 ---EGEK-----VSAYVLRLETLRRRA-----VEKRAIPRRRIADQVRL 81
DB 390 KLLGEETRLSFTSGSLITGYSSQSVGRSAVGLQTSSYLMSTRSPSYTSHVQEE 449
QY 82 QVMAGATLNQMLWCRLELKDQPPSPFLMLKVIREE-----EEEEASF 126
DB 450 QIEVRETIETIA--AKAEAKDE--PPSEGEAEKEKEKEAEAEAEAEAEAE 504
QY 127 ENESIEPEERDYGGRWNHE 146
DB 505 KESEAEKEEGEGEGEGEE 524

RESULT 5

S07144
neurofilament triplet L protein - human
N:Alternate names: neurofilament light polypeptide (68K)
N:Contains: Glu-50 brain peptide
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 21-Jul-2000
C:Accession: S07144; I52832; A60703
R:Julien, J.P.; Grosfeld, F.; Yazdankhah, K.; Flavell, D.; Meijer, D.; Mushynski, W.
Biochim. Biophys. Acta 909, 10-20, 1987
A:Title: The structure of a human neurofilament gene (NF-L): a unique exon-intron organ
A:Reference number: S07144; MUID:87214213; PMID:3034332
A:Accession: S07144
A:Molecule type: DNA
A:Residues: 1-544 <JUL>
A:Cross-references: EMBL:X05608; NID:G1495072; PID:CAA29097.1; PID:G1279504
A>Note: the authors translated the codon ATG for residue 366 as Asn
R:Postelov, V.A.; Pospelova, T.V.; Julien, J.P.
Cell Growth Differ. 5, 187-196, 1994
A:Title: AP-1 and Krox-24 transcription factors activate the neurofilament light gene p
A:Reference number: I52832; MUID:94235564; PMID:8180132
A:Accession: I52832
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-10 <POS>
A:Cross-references: GB:S70309; NID:g547176; PIDN:AAD14057.1; PID:g4261757
R;Nomata, Y.; Watanabe, T.; Wada, H.
J. Biochem. 93, 825-831, 1993
A:Title: Highly acidic proteins from human brain: purification and properties of Glu-50
A:Reference number: A60703; MUID:83265667; PMID:6135695
A:Accession: A60703
A:Molecule type: protein
A:Residues: 469-472, 'D', 474 <NOM>
A:Experimental source: Glu-50 brain peptide
A:Note: this acidic protein is named for its greater than fifty per cent glutamic acid c
C:Genetics:
A:Gene: GDB:NBFL; NFL
A:Cross-references: GDB:120227; OMIM:162280
A:Map position: 9p21-8p21
A:Introns: 349/3; 391/2; 498/1
C:Superfamily: cytoskeletal keratin
C:Keywords: brain; coiled coil; intermediate filament
F;469-544/Product: Glu-50 peptide #status predicted <B50>

Query Match 12.2%; Score 93.5; DB 2; Length 544;
Best Local Similarity 23.1%; Pred. No. 2.6;
Matches 45; Conservative 24; Mismatches 71; Indels 55; Gaps 8;

QY 2 LMHIQADNPISVEECLEAFKQVFGSLESRRTAQVRYLKPQE-----45
Db 334 LQELLEDKQNDISAMQ--DTINKLENELRITKSEMARYLKEYQDLLNVKQWALDIEIAAYR 391
QY 46 ---EGEK-----VSAYVLRLETLRRA-----VEKRAIRIADQVRLE 81
Db 392 KLLGEETRLSFTSVGTSITSCYSSQVFGSAVGGIQTSSYLMSTSFPSYITSHVQEE 451
QY 82 QVWAGATLQMLWCRRLRELKQDQPPGFLELMKVIREE-EEEEASFENESIEE-----P 134
Db 452 QTEVEETIEA---SKAEAKDEPSEGEAEKEEKEEAEAEAEAEAEAEAEAEAEAEAE 508

QY 135 EERDGYGRWNHGDD 149
Db 509 EEEGEG---EEGEE 520

RESULT 6
T14900
condensin XCAP-D2 chain - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 25-Aug-2003
C:Accession: T14900
R;Kimura, K.; Hirano, M.; Kobayashi, R.; Hirano, T.
Science 282, 487-490, 1998
A:Title: Phosphorylation and activation of 13S condensin by cdc2 in vitro.
A:Reference number: Z18257; MUID:98447791; PMID:9774278
A:Accession: T14900
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1364 <KIM>
A:Cross-references: EMBL:AF067969; NID:g3764086; PID:g3764087; PIDN:AAC64359.1
C:Superfamily: chromosome condensation complex Condensin, subunit D2

Query Match 12.2%; Score 93.5; DB 2; Length 1364;
Best Local Similarity 22.3%; Pred. No. 7.3;
Matches 35; Conservative 26; Mismatches 45; Indels 51; Gaps 6;

QY 30 ESRTAQVRYLKPQEGEKVSAVLR-LBTLRRAVEKRAIP-RRIADQVRLE-----81
Db 352 EAEKSSRDQFLDTLQELHVDVNTVRSVCVQIYNRIQVEXALPLSRFSQSVTLVWGLRFD 411
QY 82 -----QVWAGATLQMLACRL-----RELKD-----QGPP-----106
Db 412 KSNVCKNAIQLLASFLANNPFTKLSVDLKVPLEKETKLLKEMREKYQGPKPFWVVISP 471
QY 107 -----PSFLELMKVIREEEAEASFENESIEEPE 135

Db 472 EEEWEAMLPVLEAFKILQKESKEEDIEETEIESSQ 508

RESULT 7
G72253
RNA polymerase sigma-A factor - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: G72253
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: G72253
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-399 <ARN>
A:Cross-references: GB:AE001796; GB:AE000512; NID:g4982004; PIDN:AAD36519.1; PID:g498201
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1451
C:Superfamily: transcription initiation factor sigma 43; transcription initiation factor
F;161-387/Domain: transcription initiation factor sigma katF homology <KTF>

Query Match 12.1%; Score 93; DB 2; Length 399;
Best Local Similarity 22.4%; Pred. No. 2;
Matches 44; Conservative 31; Mismatches 63; Indels 58; Gaps 6;

QY 1 DLMIHQADNPIS---SVEECLEAFKQVFGSLESRRTAQVRYLKPQEGEKVSAVLR 56
Db 101 ELBELLEKESPEIHDSNVSDSIKMYLKEIGKIPLLTPAQERLARAAQMGDKKAKELI 160
QY 57 LETL-----LRRAVEK-----RAIP 71
Db 161 TSNLRVVSIAKRYMGRGLSFQDLIQEGNIGLLKAVEKFDWRKGYKSTVATWIRQAIT 220
QY 72 RRIADQVRLEQVMAG--ATLNQMLWCRRLRELKQDQPPGFLELMKVIREEEEE---EA 124
Db 221 RAIAQDQARTIRIPVHMVETINKLNRREYVQKHGEPSTIEELAKMGKPKKIKILEA 280

QY 125 SFENESIEEP--EERD 138
Db 281 AKETISLESPIGEDED 296

RESULT 8
S32739
filensin - chicken
C:Species: Gallus gallus (chicken)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Sep-1997
C:Accession: S32739
R;Remington, S.G.
submitted to the EMBL Data Library, March 1993
A:Description: Chicken filensin: a lens fiber cell protein exhibits sequence similarity t
A:Reference number: S32739
A:Accession: S32739
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-657 <REM>
A:Cross-references: EMBL:X72873; NID:g296208; PID:g296209

Query Match 11.9%; Score 91; DB 2; Length 657;
Best Local Similarity 25.7%; Pred. No. 5.2;
Matches 37; Conservative 29; Mismatches 50; Indels 28; Gaps 6;

QY 20 EAFKQVFGSLESRRTAQVRYLKPQEGEKVSAVLR-----ETLLRRAVEKRAIPRR 73
Db 19 DAYDELRGSPFSDSLAQAGLENLQELNERFASYNRVARVLEQRNLTILRKQLETF---QR 75
QY 74 IADQVRLEQVMAG--ATLNQMLWCRRLRELKQDQPPGFLELMKVIREE-----BEEAS 125

Db 76 NDELVLDEAFAGQIEFNQ---RMRELAS-----DRAKLEREKDAQRMLEDYHMK 124

QY 126 FNESEIEPEERDGYGRWNHGDD 149
: || : : : || :
Db 125 YNREYEQOKLETTLRLNKEADE 148

RESULT 9

QFMSL

N:Alternate names: 68K neurofilament protein; NF-L(low) protein; type IV IF protein
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1988 #sequence revision 30-Sep-1993 #text_change 22-Jun-1999
C:Accession: A25227; A26562; A43772; A41012; 155316
R:Lewis, S.A.; Cowan, N.J.
Mol. Cell. Biol. 6, 1529-1534, 1986
A:Title: Anomalous placement of introns in a member of the intermediate filament multigene family
A:Reference number: A25227; MUID:87064433; PMID:3785173
A:Accession: A25227
A:Molecule type: DNA
A:Residues: 1-543 <LEW>
A:Cross-references: GB:M13016; NID:G200023; PIDN:AAA39810.1; PID:G387492
A:Note: The authors translated the codon GGC for residue 5 as Ala, ACA for residue 88 as 1 as Glu

R:Lewis, S.A.; Cowan, N.J.
J. Cell Biol. 100, 843-850, 1985
A:Title: Genetics, evolution, and expression of the 68,000-mol-wt neurofilament protein:
A:Reference number: A26562; MUID:85131334; PMID:3919033
A:Accession: A26562
A:Molecule type: mRNA
A:Residues: 242-543 <LB2>
A:Cross-references: GB:X02165
A:Experimental source: brain
R:Julien, J.P.; Meyer, D.; Flavell, D.; Hurst, J.; Grosveld, F.
Brain Res. Mol. Brain Res. 1, 243-250, 1986
A:Title: Cloning and developmental expression of the murine neurofilament gene family.
A:Reference number: A43772
A:Accession: A43772
A:Molecule type: mRNA
A:Residues: 1-5, 'Y', 7-8, 'Y', 10-64, 'M', 66-72, 'L', 74-98, 'D', 100-194, 'R', 196-202, 204-239, 'Y'
A:Cross-references: GB:M20480; NID:G200037; PIDN:AAA39814.1; PID:G200038
A:Note: The authors translated the codon CGC for residue 195 as Ala
R:Sihaq, R.K.; Nixon, R.A.
J. Biol. Chem. 266, 18861-18867, 1991
A:Title: Identification of Ser-55 as a major protein kinase A phosphorylation site on the
A:Reference number: A41012; MUID:92011653; PMID:1717455
A:Accession: A41012
A:Molecule type: protein
A:Residues: 52-57 <SIH>
R:Nakahira, K.; Ikenaka, K.; Wada, K.; Tamura, T.
J. Biol. Chem. 265, 19786-19791, 1990
A:Title: Structure of the 68-kDa neurofilament gene and regulation of its expression.
A:Reference number: I55316; MUID:91060592; PMID:2246261
A:Accession: I55316
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-5, 'Y', 7-8, 'Y', 10-28 <RES>
A:Cross-references: GB:M55423; NID:G200027; PIDN:AAA39812.1; PID:G554245
C:Comment: This is the most abundant of the three neurofilament proteins and, as the other two, is a major component of the cytoskeleton
C:Genetics:
A:Introns: 349/3; 391/2; 498/1
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:2-72/Domain: head <HED>
F:94-125/Domain: coil 1a, alpha-helical rod #status predicted <R1A>
F:126-138/Region: linker 1
F:139-234/Domain: coil 1b, alpha-helical rod #status predicted <R1B>
F:235-256/Region: linker 12
F:257-272/Domain: coil 2a, alpha-helical rod #status predicted <R2A>
F:273-281/Region: linker 2
F:282-401/Domain: coil 2b, alpha-helical rod #status predicted <R2B>
F:404-543/Domain: tail <TAI>
F:404-444/Region: tail subdomain a

F:445-543/Region: tail subdomain b

Query Match 11.7%; Score 90; DB 1; Length 543;
Best Local Similarity 22.4%; Pred. No. 5.1;
Matches 44; Conservative 26; Mismatches 66; Indels 60; Gaps 8;

QY 2 LMHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRVILKPYQE----- 45
: || : : : || :
Db 334 LOELEDKQNDISAMQ--DTINKLENELESTSEMARYLKEYQDLLNVKALDIEIAAYR 391

QY 46 ---EGEK-----VSAYVLRLTLRRA-----VEKRAIPRIADQVRLE 81
||| : : : ||| :
Db 392 KLEGEETRSLPTSQSGTSITSGYSQSQVGRGAYSGLOSSYLMGARSPPAYTTSVQVEE 451

QY 82 QVMAGATLNQMLWCRLRLKLDQGGPPSPFLMKVIREEE-----EEASFENESIEE 133
: || : : : ||| : : : ||| : : : ||| :
Db 452 QTEVETIEA--TKAEAKDE--PFSEGEAEERKEKEEGEEGAEEERAAKDESDT 506

QY 134 PEERDGYGRWNHGDD 149
|| : || : || :
Db 507 KEEREG-----GEGEE 517

RESULT 10

JC7709

testis-specific kinase substrate protein - human
C:Species: Homo sapiens (man)
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
R:Scorillas, A.; Yousef, G.M.; Jung, K.; Rajpert-De Meyts, E.; Carsten, S.; Diamandis, E.
Biochem. Biophys. Res. Commun. 285, 400-408, 2001
A:Title: Identification and characterization of a novel human testis-specific kinase sub
A:Reference number: JC7709; MUID:21338223; PMID:11444856
A:Accession: JC7709
A:Molecule type: DNA
A:Residues: 1-532 <SCO>
A:Cross-references: GB:AF200923
C:Comment: This protein, a homolog of mouse testis-specific serine kinase substrate prot
a role in testicular pathologies. It plays a role in the pathogenesis of Digeorge and v
C:Genetics:
A:Gene: tsks
A:Map position: 19q13.3
A:Introns: 57/2; 133/3; 165/3; 193/3; 221/3; 331/2; 396/2; 454/2; 499/3; 541//2
F:1-19/Domain: hydrophobic signal sequence #status predicted <SIG>

Query Match 11.7%; Score 90; DB 2; Length 592;
Best Local Similarity 24.0%; Pred. No. 5.6;
Matches 35; Conservative 30; Mismatches 67; Indels 14; Gaps 3;

QY 5 IYQADNPSISVEECLEAFKQVFGSLESRRTAQVRVILKPYQEGRKVSAYVLRLLET---LL 61
: || : : : ||| : : : ||| : : : ||| :
Db 140 IYRAKDSITSLEKTNVNHQVQSQSECSVLSENLRERQAEAELEGYCIQLKENCWKV 199

QY 62 RRAVEKRAIPRIADQVRLEQVMAGATLNQMLWCRLRLKLDQGGPPSPFLMKVIREEE 121
: || : : : ||| : : : ||| : : : ||| :
Db 200 TRSVDAAIKTNVLKQ-----NSALLEKRLYQQQLQDETTPRQEAEL-----QEPEE 248

QY 122 EEASFENESIEEPEERDGYGRWNHEG 147
: || : : : ||| : ||| :
Db 249 KOEPEEKQPEBKQPEAGLSWNSLG 274

RESULT 11

T00034

SARR-1 protein - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C:Accession: T00034
R:Shichiyo, S.; Nakao, M.; Inai, Y.; Takasu, H.; Kawamoto, M.; Niiya, F.; Yang, D.; Toh,
J. Exp. Med. 187, 277-288, 1998
A:Title: A gene encoding antigenic peptides of human squamous cell carcinoma recognized
A:Reference number: Z14071; MUID:98119878; PMID:9449708
A:Accession: T00034

C; Superfamily: Rhodobacter sphaeroides protoporphyrin IX magnesium chelatase bchD

RESULT 13

R;Vornlocher, H.; Sprinzl, M.

RESULT 15

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 27, 2004, 17:10:17 ; Search time 43.3366 Seconds
(without alignments)
1105.584 Million cell updates/sec

Title: US-10-037-860-9
Perfect score: 766
Sequence: 1 DLHIVQADNPSISVECLE.....SIEPEERDGYGRWNHEGDD 149

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1349238 seqs, 32158718 residues

Total number of hits satisfying chosen parameters: 1349238

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pap:*
- 2: /cgn2_6/ptodata/2/pubaa/PTCT_NEW_PUB.pap:*
- 3: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB.pap:*
- 4: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB.pap:*
- 5: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB.pap:*
- 6: /cgn2_6/ptodata/2/pubaa/PTCTUS_PUBCOMB.pap:*
- 7: /cgn2_6/ptodata/2/pubaa/US08_NEW_PUB.pap:*
- 8: /cgn2_6/ptodata/2/pubaa/US08_PUBCOMB.pap:*
- 9: /cgn2_6/ptodata/2/pubaa/US09A_PUBCOMB.pap:*
- 10: /cgn2_6/ptodata/2/pubaa/US09B_PUBCOMB.pap:*
- 11: /cgn2_6/ptodata/2/pubaa/US09C_PUBCOMB.pap:*
- 12: /cgn2_6/ptodata/2/pubaa/US09D_NEW_PUB.pap:*
- 13: /cgn2_6/ptodata/2/pubaa/US10A_PUBCOMB.pap:*
- 14: /cgn2_6/ptodata/2/pubaa/US10B_PUBCOMB.pap:*
- 15: /cgn2_6/ptodata/2/pubaa/US10C_PUBCOMB.pap:*
- 16: /cgn2_6/ptodata/2/pubaa/US10_NEW_PUB.pap:*
- 17: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB.pap:*
- 18: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	766	100.0	149	13	US-10-037-860-9
2	755	98.6	283	13	US-10-037-860-11
3	323	42.2	463	13	US-10-037-860-13
4	295.5	38.6	353	9	US-09-965-529-7
5	295.5	38.6	353	10	US-09-969-680A-7
6	287	37.5	452	16	US-10-408-765A-2385
7	277	36.2	399	15	US-10-094-749-1978
8	271.5	35.4	351	9	US-09-965-529-1
9	271.5	35.4	351	10	US-09-969-680A-1
10	271.5	35.4	351	12	US-09-804-014A-16
11	271.5	35.4	351	15	US-10-341-434-10
12	256.5	33.5	329	13	US-10-037-860-4
13	255	33.3	318	12	US-09-804-014A-40
14	247.5	32.3	403	15	US-10-094-466-38
15	240	31.3	337	12	US-10-296-115-1208

16	235	30.7	321	12	US-09-804-014A-39	Sequence 39, Appl
17	225	29.4	312	12	US-09-804-014A-73	Sequence 73, Appl
18	225	29.4	312	12	US-09-804-014A-74	Sequence 74, Appl
19	97.5	12.7	218	15	US-10-094-749-2881	Sequence 2881, Ap
20	96.5	12.6	542	12	US-10-205-331-57	Sequence 57, Appl
21	95.5	12.5	407	16	US-10-755-889-122	Sequence 122, App
22	93.5	12.2	620	16	US-10-437-963-158544	Sequence 158544,
23	91.5	11.9	346	15	US-10-310-154-448	Sequence 448, App
24	90	11.7	592	12	US-10-416-477-8	Sequence 8, Appli
25	89	11.6	592	12	US-10-438-339-8	Sequence 8, Appli
26	89	11.6	1474	16	US-10-437-963-187531	Sequence 187531,
27	87.5	11.4	2552	16	US-10-437-963-129734	Sequence 129734,
28	87	11.4	545	9	US-09-908-988B-4	Sequence 4, Appli
29	87	11.4	545	16	US-10-775-649-4	Sequence 4, Appli
30	87	11.4	545	16	US-10-775-627-4	Sequence 4, Appli
31	84.5	11.0	1300	16	US-10-408-765A-257	Sequence 257, App
32	83	10.8	882	14	US-10-298-417-2	Sequence 2, Appli
33	83	10.8	1687	16	US-10-437-963-187527	Sequence 187527,
34	83	10.8	1708	16	US-10-437-963-187533	Sequence 187533,
35	82.5	10.8	384	16	US-10-437-963-182739	Sequence 182739,
36	82.5	10.8	435	9	US-09-866-582-33	Sequence 33, Appl
37	82.5	10.8	549	16	US-10-437-963-156505	Sequence 156505,
38	82.5	10.8	817	12	US-10-363-616-447	Sequence 447, App
39	82.5	10.8	996	16	US-10-380-492A-4	Sequence 4, Appli
40	82.5	10.8	1002	16	US-10-380-492A-2	Sequence 2, Appli
41	82.5	10.8	1009	14	US-10-290-544-2	Sequence 2, Appli
42	82.5	10.8	1009	14	US-10-290-544-5	Sequence 5, Appli
43	82.5	10.8	1023	15	US-10-108-260A-3123	Sequence 3123, Ap
44	82.5	10.8	1023	16	US-10-380-492A-8	Sequence 8, Appli
45	82	10.7	715	16	US-10-408-765A-2096	Sequence 2096, Ap

ALIGNMENTS

RESULT 1
US-10-037-860-9
; Sequence 9, Application US/10037860
; Publication No. US20020123114A1
; GENERAL INFORMATION:
; APPLICANT: Jerome B. Posner
; APPLICANT: Josep O. Dalmau
; APPLICANT: Myrna R. Rosenfeld
; TITLE OF INVENTION: Ma FAMILY POLYPEPTIDES AND ANTI-Ma
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 2581.1004-004
; CURRENT APPLICATION NUMBER: US/10/037,860
; CURRENT FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 09/189,527
; PRIOR FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 149
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-037-860-9

Query Match	100.0%;	Score 766;	DB 13;	Length 149;
Best Local Similarity	100.0%;	Pred. No. 2.9e-71;		
Matches 149;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	DLHIVQADNPSISVECLEAFQVFGSLSRRTAQVRLKPYQEGEKVSAYVRLLETL	60	
Db	1	DLHIVQADNPSISVECLEAFQVFGSLSRRTAQVRLKPYQEGEKVSAYVRLLETL	60	
Qy	61	LRRAVEKATPRIADQVRLQVWAGTTLNQLWCLRELKDCGPPPSFLELMKVIREEE	120	
Db	61	LRRAVEKATPRIADQVRLQVWAGTTLNQLWCLRELKDCGPPPSFLELMKVIREEE	120	
Qy	121	EEBASFNESIEEPEDRDGYGRWNHEGDD	149	
Db	121	EEBASFNESIEEPEDRDGYGRWNHEGDD	149	

RESULT 2

US-10-037-860-11

; Sequence 11, Application US/10037860

; Publication No. US20020123114A1

; GENERAL INFORMATION:

; APPLICANT: Jerome B. Posner

; APPLICANT: Josep O. Dalmau

; APPLICANT: Myrna R. Rosenfeld

; TITLE OF INVENTION: Ma FAMILY POLYPEPTIDES AND ANTI-Ma

; TITLE OF INVENTION: ANTIBODIES

; FILE REFERENCE: 2581.1004-004

; CURRENT APPLICATION NUMBER: US/10/037,860

; PRIOR FILING DATE: 2001-01-04

; PRIOR FILING DATE: 1998-11-10

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11

; LENGTH: 283

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-037-860-11

Query Match

Best Local Similarity 98.6%; Score 755; DB 13; Length 283;

Matches 147; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY

1 DLMHIVQADNPSISVEECLEAFKQVFGSLESRTAQVRLKPYQEGEKVSAYVLRLETL 60

DB

135 DLMHIVQADNPSISVEECLEAFKQVFGSLESRTAQVRLKPYQEGEKVSAYVLRLETL 194

QY

61 LRRAVEKRAIPRIADQVRLQVMAGATLQMLWCRLRELKDQGPSPFLELMKVIRLEE 120

DB

195 LKAVEKRAIPRIADQVRLQVMAGATLQMLWCRLRELKDQGPSPFLELMKVIRLEE 254

QY

121 EEEASFENESIEPEPERDGYGRWNHEGDD 149

DB

255 EEEASFENESIEPEPERDGYGRWNHEGDD 283

RESULT 3

US-10-037-860-13

; Sequence 13, Application US/10037860

; Publication No. US20020123114A1

; GENERAL INFORMATION:

; APPLICANT: Jerome B. Posner

; APPLICANT: Josep O. Dalmau

; APPLICANT: Myrna R. Rosenfeld

; TITLE OF INVENTION: Ma FAMILY POLYPEPTIDES AND ANTI-Ma

; TITLE OF INVENTION: ANTIBODIES

; FILE REFERENCE: 2581.1004-004

; CURRENT APPLICATION NUMBER: US/10/037,860

; CURRENT FILING DATE: 2001-01-04

; PRIOR APPLICATION NUMBER: 09/189,527

; PRIOR FILING DATE: 1998-11-10

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13

; LENGTH: 463

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-037-860-13

Query Match

Best Local Similarity 42.2%; Score 323; DB 13; Length 463;

Matches 68; Conservative 26; Mismatches 33; Indels 2; Gaps 1;

QY

6 VOADNPSISVEECLEAFKQVFGSLESRTAQVRLKPYQEGEKVSAYVLRLETLRRAV 65

DB

220 LRASNASIVECLALQVFGVESHKTAQVKLCKAYQEGEKVSFVLRLEPLQRAV 279

QY 66 EKRAIPRIADQVRLQVMAGATLQMLWCRLRELKDQGPSPFLELMKVIRREEEAS 125
DB 280 ENNVSRNVNQTRLKRVLSGATLPDKLRDKUMKQRKPGCFALVAKLREEWEEAT 339
QY 126 F--ENESIE 132
DB 340 LGPDRESLE 348

RESULT 4

US-09-965-529-7

; Sequence 7, Application US/09965529

; Publication No. US20020182671A1

; GENERAL INFORMATION:

; APPLICANT: LAL, Preeti

; APPLICANT: YUE, Henry

; APPLICANT: TANG, Y. Tom

; APPLICANT: BANDMAN, Olga

; APPLICANT: BURFORD, Neil

; APPLICANT: AZIMZAI, Yalda

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: LU, Dyung Aina M.

; APPLICANT: PATTERSON, Chandra

; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS

; FILE REFERENCE: PF-0731 USA

; CURRENT APPLICATION NUMBER: US/09/965,529

; PRIOR FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315

; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PERL Program

; SEQ ID NO 7

; LENGTH: 353

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. US20020182671A1 2483172CD1

US-09-965-529-7

Query Match

Best Local Similarity 38.6%; Score 295.5; DB 9; Length 353;

Matches 62; Conservative 29; Mismatches 36; Indels 7; Gaps 2;

QY

1 DLMHIVQADNPSISVEECLEAFKQVFGSLESRTAQVRLKPYQEGEKVSAYVLRLETL 60

DB

212 DVIRILKSNPAITTAETACLEKALEQVFGSVESRDAQIKFLNTYQNPGEKLSAYVIRLEPL 271

QY

61 LRRAVEKRAIPRIADQVRLQVMAGATLQMLWCRLRELKDQGPSPFLELMKVIR 116

DB

272 LQKVEKGAIDKDNVQARLEQVIAGANHSQAIRQLML---TGAGEGPAPNLFQLLVQI 328

QY

117 REEEERASFENES 130

DB

329 REEEERAEAEAE 342

RESULT 5

US-09-969-680A-7

; Sequence 7, Application US/09969680A

; Publication No. US20030124649A1

; GENERAL INFORMATION:

; APPLICANT: LAL, Preeti; YUE, Henry

; APPLICANT: TANG, Y. Tom; BANDMAN, Olga

; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda

; APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.

; APPLICANT: PATTERSON, Chandra

; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS

; FILE REFERENCE: PF-0731-1 USA

; CURRENT APPLICATION NUMBER: US/09/969,680A

; PRIOR FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US00/22315

; PRIOR FILING DATE: 2000-08-14


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; PRIOR APPLICATION NUMBER: 60/149,641
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/164,203
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: incyte ID No. US20030124649A1 2483172CD1
US-09-969-680A-7

Query Match      38.6%; Score 295.5; DB 10; Length 353;
Best Local Similarity 46.3%; Pred. No. 4.8e-22;
Matches 62; Conservative 29; Mismatches 36; Indels 7; Gaps 2;

Qy 1 LMHIQADNPSISVEECLEAFKQVFGSLESRRTAQVRLKPYQEEGKVSAYVRLLETL 60
Db 212 DVIRILKSNPAITAECLKALEQVFGSVSSRDAQIKFLNTYQNGEKL SAYVIRLEPL 271
Qy 61 LRAVEKRAIPRIADQVRLEOVWAGA----TLNQLWCRLRELKDGPPSPFLELMKVI 116
Db 272 LQKVEKATDKUNVQARLEQVIAGNHSAIRQLWL----TGAGGPAFNLQFLLVQI 328
Qy 117 REEEEEEASFENES 130
Db 329 REEAKKEEEEA 342

RESULT 6
US-10-408-765A-2385
; Sequence 2385, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; CURRENT APPLICATION NUMBER: 660088.465
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2385
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2385

Query Match      37.5%; Score 287; DB 16; Length 452;
Best Local Similarity 43.8%; Pred. No. 5e-21;
Matches 63; Conservative 30; Mismatches 43; Indels 8; Gaps 2;

Qy 2 LMHIQADNPSISVEECLEAFKQVFGSLESRRTAQVRLKPYQEEGKVSAYVRLLETL 61
Db 215 IMRVLQANDNSITVEQCILDALKIFGDKEDFRASQFRPLQTSPIKIGEKVSTFLRLEPL 274
Qy 62 RRAVEKRAIPRIADQVRLEOVWAGATLNQMLWCRLRELKDGPPSPFLELMKVIREEE 121
Db 275 QKAVEKPLSVSRDMDLRLKHLARVMTPLRKLLELDQRCPPNFLELMKLIIRDEE 334
Qy 122 ---EEASFENESIEEPEERDGYGR 142
Db 335 WENTEAVMKNK-----EKPSGRGR 353
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```
RESULT 7
US-10-094-749-1978
; Sequence 1978, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1978
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-1978

Query Match      36.2%; Score 277; DB 15; Length 399;
Best Local Similarity 43.5%; Pred. No. 4.6e-20;
Matches 60; Conservative 30; Mismatches 48; Indels 0; Gaps 0;

Qy 2 LMHIQADNPSISVEECLEAFKQVFGSLESRRTAQVRLKPYQEEGKVSAYVRLLETL 61
Db 208 LVHALLAENPARTAQDCIALLAQVFGDNESQATIRVKCLTAQQQSGERLSAFVLRLEVL 267
Qy 62 RRAVEKRAIPRIADQVRLEOVWAGATLNQMLWCRLRELKDGPPSPFLELMKVIREEE 121
Db 268 QKAVEKALARASADRVRLRQMLTRAHLTEPLDEALRLRMAGRSPSFLEMLGLVRESEA 327
Qy 122 EEASFENESIEEPEERDQ 139
Db 328 WEASLARSVRAQTQEGAG 345

RESULT 8
US-09-965-529-1
; Sequence 1, Application US/09965529
; Publication No. US20020182671A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yaida
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731 USA
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; CURRENT APPLICATION NUMBER: US/09/965,529
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 112301CD1
US-09-965-529-1

Query Match      35.4%; Score 271.5; DB 9; Length 351;
Best Local Similarity 44.6%; Pred. No. 1.5e-19;
Matches 58; Conservative 32; Mismatches 29; Indels 11; Gaps 3;

Qy      1  DLMHIQVADNPISVBECLAFQVFGSLESRTAQVRYLKPQYBEGEKVSAYVLRLETL 60
Db      216 DVIRLKIKNPLITVDECIQALBEVFGVTDPRELQVKYLTYYQDDEKLSAYVLRLEPL 275

Qy      61  LRRAVEKRAIPRIADQVRLEQVMAGA---TLNQMLWCRLRELKQDQPPSPFLELMKVIR 117
Db      276 LQKLVQGAERDAVNQARLDQVIAGVHKTIIRREL-----NLPEDGAPGFLQLLVLIK 330

Qy      118 E---EEEEEA 124
Db      331 DYEAEEEEEA 340

RESULT 9
US-09-969-680A-1
; Sequence 1, Application US/09969680A
; Publication No. US20030124649A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti; YUE, Henry
; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.; LU, Dying Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731-1 USA
; CURRENT APPLICATION NUMBER: US/09/969,680A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US00/22315
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/149,641
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/164,203
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124649A1 112301CD1
US-09-969-680A-1

Query Match      35.4%; Score 271.5; DB 10; Length 351;
Best Local Similarity 44.6%; Pred. No. 1.5e-19;
Matches 58; Conservative 32; Mismatches 29; Indels 11; Gaps 3;

Qy      1  DLMHIQVADNPISVBECLAFQVFGSLESRTAQVRYLKPQYBEGEKVSAYVLRLETL 60
Db      216 DVIRLKIKNPLITVDECIQALBEVFGVTDPRELQVKYLTYYQDDEKLSAYVLRLEPL 275

Qy      61  LRRAVEKRAIPRIADQVRLEQVMAGA---TLNQMLWCRLRELKQDQPPSPFLELMKVIR 117

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; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-341-434-10

Query Match 35.4%; Score 271.5; DB 15; Length 351;
Best Local Similarity 44.6%; Pred. No. 1.5e-19;
Matches 58; Conservative 32; Mismatches 29; Indels 11; Gaps 3;

QY 1 DLHIVQADNPISVERCLEAFKQVFGSLERRTAQVRYLKPQYEEGKVSAYVLRLETL 60
Db 216 DVIRLKSNNPAITTAELKALEQVFGSVESRDQAQIKFLNTYQNPGEKLSAYVIRLEPL 275
QY 61 LRAVEKRAIPRRIADQVRLEQVWAGA---TLNQMLWCRLRELKDDQPPPSFLEIMKVIR 117
Db 276 LQKLVQGAERDAVNOARLDQVIAGVHKTRREL-----NLPEDGAPGFLQLLVLIK 330
QY 118 E---EEBEEA 124
Db 331 DYEAABEEBA 340

RESULT 12
US-10-037-860-4
; Sequence 4, Application US/10037860
; Publication No. US20020123114A1
; GENERAL INFORMATION:
; APPLICANT: Jerome B. Posner
; APPLICANT: Joseph O. Dalmay
; APPLICANT: Wynna R. Rosenfeld
; TITLE OF INVENTION: Ma FAMILY POLYPEPTIDES AND ANTI-Ma
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 2581.1004-004
; CURRENT APPLICATION NUMBER: US/10/037,860
; CURRENT FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 09/189,527
; PRIOR FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 329
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-037-860-4

Query Match 33.5%; Score 256.5; DB 13; Length 329;
Best Local Similarity 46.6%; Pred. No. 4.8e-18;
Matches 54; Conservative 25; Mismatches 30; Indels 7; Gaps 2;

QY 1 DLHIVQADNPISVERCLEAFKQVFGSLERRTAQVRYLKPQYEEGKVSAYVLRLETL 60
Db 212 DVIRLKSNNPAITTAELKALEQVFGSVESRDQAQIKFLNTYQNPGEKLSAYVIRLEPL 271
QY 61 LRAVEKRAIPRRIADQVRLEQVWAGA---TLNQMLWCRLRELKDDQPPPSFLEL 112
Db 272 LQKVVEKGAIDKDNVNOARLEQVIAGANHSGAIRRLQLW---TGAGRGPGKPLSV 324

RESULT 13
US-09-804-014A-40
; Sequence 40, Application US/09804014A
; Publication No. US20030064489A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard
; APPLICANT: Spaderna, Steven

; APPLICANT: Majumder, Kumud
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-721 US
; CURRENT APPLICATION NUMBER: US/09/804,014A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/189,316
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/189,277
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/189,139
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: 60/189,140
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: 60/190,401
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/190,231
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (20)
; OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
; OTHER INFORMATION: specification
US-09-804-014A-40

Query Match 33.3%; Score 255; DB 12; Length 318;
Best Local Similarity 51.0%; Pred. No. 6.5e-18;
Matches 50; Conservative 23; Mismatches 21; Indels 4; Gaps 1;

QY 1 DLHIVQADNPISVERCLEAFKQVFGSLERRTAQVRYLKPQYEEGKVSAYVLRLETL 60
Db 212 DVIRLKSNNPAITTAELKALEQVFGSVESRDQAQIKFLNTYQNPGEKLSAYVIRLEPL 271
QY 61 LRAVEKRAIPRRIADQVRLEQVWAGA---TLNQMLW 94
Db 272 LQKVVEKGAIDKDNVNOARLEQVIAGANHSGAIRRLQLW 309

RESULT 14
US-10-094-466-38
; Sequence 38, Application US/10094466
; Publication No. US2003020363A1
; GENERAL INFORMATION:
; APPLICANT: SpYtek et al.
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM
; TITLE OF INVENTION: AND METHODS OF USING
; TITLE OF INVENTION: THE SAME
; FILE REFERENCE: 21402-290D
; CURRENT APPLICATION NUMBER: US/10/094,466
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/288,148
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/275,235
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/338,375
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/275,579
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/335,302
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/275,601
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/276,000
; PRIOR FILING DATE: 2001-03-14

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; PRIOR APPLICATION NUMBER: 60/277,338
; PRIOR FILING DATE: 2001-03-20
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patin 2.1
; SEQ ID NO 38
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-466-38

Query Match      32.3%; Score 247.5; DB 15; Length 403;
Best Local Similarity 42.0%; Pred. No. 5.3e-17;
Matches 55; Conservative 28; Mismatches 43; Indels 5; Gaps 1;

QY 1 DLMHIVQADNPISIVVEECLEAFKQVFGSLERRTAQVRYLKPQYEEGKVSAYVLRLETL 60
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
96 EVMRLQANPNLSVADFLRAMKLVFGESSESVTAHGKFFNTLQAQGEKASLYVIRLEVQ 155

QY 61 LRAVEKRAIPRIADQVLEQVMAGATLNQMLWCRLREL-----KDQGPSPSFLMLMKV 115
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
156 LQNAIQAGIIAEKDANRTLQQLLGAGLNRLDFRLKHLRLMYANKQERLPNFLELIKM 215

QY 116 IREEEEEASF 126
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
216 IREEDWDADF 226

RESULT 15
US-10-296-115-1208
; Sequence 1208, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1208
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1208

Query Match      31.3%; Score 240; DB 12; Length 337;
Best Local Similarity 37.2%; Pred. No. 2.5e-16;
Matches 54; Conservative 34; Mismatches 45; Indels 12; Gaps 2;

QY 1 DLMHIVQADNPISIVVEECLEAFKQVFGSLERRTAQVRYLKPQYEEGKVSAYVLRLETL 60
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
80 EVMRLQATNPNSVADFLRAMKLVFGESSESVTAHGKFFNTLQAQGEKASLYVIRLEVQ 139

QY 61 LRAVEKRAIPRIADQVLEQVMAGATLNQMLWCRLREL-----KDQGPSPSFLMLMKV 115
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
140 LQNAIQAGIIAEKDANRTLQQLLGAGLSRDLRLKDFLRMYANEQERLPNFLELIKM 199

QY 116 IREEEEEASF-----ENESIEE 133
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
200 VREEDWDADFIRKRPKRSSESMVE 224
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Search completed: September 27, 2004, 17:26:04
Job time : 44.3366 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 17:06:36 ; Search time 7.54739 Seconds
(without alignments)
1019.197 Million cell updates/sec

Title: US-10-037-860-9

Perfect score: 766

Sequence: 1 DLMHIVQADNPISVVECLE.....SIEPERDGYGRWNHEGDD 149

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pap.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pap.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pap.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pap.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pap.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	323	42.2	462	4	US-09-189-527-13
2	256.5	33.5	329	4	US-09-189-527-4
3	89.5	11.7	800	4	US-09-555-790A-2
4	81.5	10.6	1898	1	US-08-056-200-94
5	81.5	10.6	1898	2	US-08-800-644-94
6	80	10.4	825	4	US-09-540-824-26
7	77	10.1	237	2	US-08-469-537A-85
8	77	10.1	370	3	US-08-857-076-107
9	77	10.1	661	4	US-09-107-532A-3677
10	77	10.1	1367	2	US-08-249-687C-2
11	77	10.1	1367	2	US-08-625-819-2
12	77	10.1	1367	3	US-08-746-559A-2
13	77	10.1	1367	4	US-08-864-641B-18
14	77	10.1	1367	4	US-09-343-551-2
15	76	9.9	754	4	US-09-585-173B-51
16	75.5	9.9	591	4	US-09-198-452A-806
17	75	9.8	571	4	US-09-489-039A-10805
18	75	9.8	704	4	US-09-370-838-191
19	75	9.8	1197	4	US-09-618-425-2
20	74	9.7	217	1	US-08-185-424B-2
21	74	9.7	322	4	US-09-540-236-2700
22	74	9.7	420	3	US-09-329-418-8
23	74	9.7	420	3	US-09-531-914-8
24	74	9.7	497	4	US-09-345-473E-8
25	74	9.7	518	3	US-09-329-418-3
26	74	9.7	518	3	US-09-329-418-4
27	74	9.7	518	3	US-09-329-418-5

28 74 9.7 518 3 US-09-329-418-9 Sequence 9, Appli
29 74 9.7 518 3 US-09-531-914-3 Sequence 3, Appli
30 74 9.7 518 3 US-09-531-914-4 Sequence 4, Appli
31 74 9.7 518 3 US-09-531-914-5 Sequence 5, Appli
32 74 9.7 518 3 US-09-531-914-9 Sequence 9, Appli
33 73.5 9.6 336 4 US-09-252-991A-24656 Sequence 24656, A
34 73.5 9.6 783 6 5231168-2 Patent No. 5231168
35 73.5 9.6 1208 4 US-09-134-000C-5756 Sequence 5756, Ap
36 73 9.5 355 4 US-09-134-001C-3622 Sequence 3622, Ap
37 73 9.5 1588 5 PCT-US93-07261-11 Sequence 11, Appl
38 73 9.5 1663 5 PCT-US93-07261-16 Sequence 16, Appl
39 73 9.5 1985 4 US-09-495-714C-6 Sequence 6, Appli
40 72.5 9.5 258 4 US-09-489-039A-12052 Sequence 12052, A
41 72.5 9.5 651 3 US-08-650-766-6 Sequence 6, Appli
42 72.5 9.5 651 3 US-08-922-635-5 Sequence 5, Appli
43 72.5 9.5 651 4 US-09-389-487-6 Sequence 6, Appli
44 72.5 9.5 1070 3 US-08-922-635-22 Sequence 22, Appl
45 72.5 9.5 1504 4 US-09-364-206-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-189-527-13
; Sequence 13, Application US/09189527A
; Patent No. 6387639

; GENERAL INFORMATION:

; APPLICANT: Jerome B. Posner

; APPLICANT: Joseph O. Dalmau

; APPLICANT: Myrna R. Rosenfeld

; TITLE OF INVENTION: Ma Family Polypeptides and Anti-Ma

; TITLE OF INVENTION: Antibodies

; FILE REFERENCE: SLK98-01

; CURRENT APPLICATION NUMBER: US/09/189,527A

; CURRENT FILING DATE: 1998-11-10

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 13

; LENGTH: 462

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-189-527-13

Query Match 42.2%; Score 323; DB 4; Length 462;

Best Local Similarity 52.7%; Pred. No. 2.9e-29;

Matches 68; Conservative 26; Mismatches 33; Indels 2; Gaps 1;

Qy 6 VQADNPISVVECLEAPKQVFGSLESRRTAQVRVLYKPYQEGEKVAYVURLETLRRAY 65

Db 214 LRASNASITVEECLAAQQVFGPVESHKIAQVKLCKAYQEGEKVSSFVLRLEPLQRAV 273

Qy 66 EKRAIPRIADQVRLEOVMAQTINQMLCRLRELKQGGPPSPFLELMKVIREEESEAS 125

Db 274 ENNVSRNVNQTRLKRVLSGATLPDKLRDKLKMQRKPPGFLALVKLUREEEWEAT 333

Qy 126 F--ENESIE 132

Db 334 LGPDRESLE 342

RESULT 2

US-09-189-527-4

; Sequence 4, Application US/09189527A

; Patent No. 6387639

; GENERAL INFORMATION:

; APPLICANT: Jerome B. Posner

; APPLICANT: Joseph O. Dalmau

; APPLICANT: Myrna R. Rosenfeld

; TITLE OF INVENTION: Ma Family Polypeptides and Anti-Ma

; TITLE OF INVENTION: Antibodies

; FILE REFERENCE: SLK98-01

; CURRENT APPLICATION NUMBER: US/09/189,527A

ADDRESS: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor

```
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: US 08/056,200
; APPLICATION NUMBER: 30-APR-1993
; FILING DATE: 30-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fredrick, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH054.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 760-0404
; TELEFAX: (714) 760-9502
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1898 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-800-644-94

Query Match          10.6%; Score 81.5; DB 2; Length 1898;
Best Local Similarity 28.9%; Pred. No. 3.9;
Matches 33; Conservative 16; Mismatches 45; Indels 25; Gaps 4;

Qy 20 EAPKQVFSLSRRTAQR---YLPKQEEGKVSAYVLRLETLRLRAVEKRAIPRIAD 76
Db 563 ERLEQLLKREERKLEQERREQLRKQEE-----REDQLLKREERQQLRKREQ 613

Qy 77 QVRLEQVMAGATNQLMWCRLRELKDGPPPSFLELMKVVIREEEERASFNESIEPPE 136
Db 614 EERLEQLRKREVERL---EQEERDE-----RLKREPEERRRHELLKSERQEE 660

Qy 137 R 137
Db 561 R 661

RESULT 6
US-09-540-824-26
; Sequence 26, Application US/09540824
; Patent No. 6383753
; GENERAL INFORMATION:
; APPLICANT: Thiele, Dennis
; TITLE OF INVENTION: Liu, Phillip
; FILE REFERENCE: UM-04266
; CURRENT APPLICATION NUMBER: US/09/540,824
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 825
; TYPE: PRP
; ORGANISM: Schizosaccharomyces pombe
; US-09-540-824-26

Query Match          10.4%; Score 80; DB 4; Length 825;
Best Local Similarity 25.8%; Pred. No. 1.8;
Matches 33; Conservative 25; Mismatches 32; Indels 38; Gaps 8;

Qy 30 ESRRTAQRYLKPQEEGKVSAYVLRLETLRLRAV-EKRAIP-RR1ADQVRLEQVMAGA 87
Db 253 KASRKSGIKTRPIISDGD-----ARYDSFVREWFDKRAHPTERTKTEELAQIAD- 305

Qy 88 TLNQLMWCRLRELKDGPPPSFLELMKVVIREEEERASFNESIEPPEERD---GYGR- 142
Db 306 -----RLRELEQD-----RISRMHYQEDSASEAGSIEDEQATDNVFGFGK 347

Qy 143 -----WN 144
Db 348 QENEENWN 355

RESULT 7
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US-08-469-537A-85
; Sequence 85, Application US/08469537A
; Patent No. 5843749
; GENERAL INFORMATION:
; APPLICANT: Maisonnier, et al.
; TITLE OF INVENTION: BHK AND ROR TYROSINE
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,537A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/406,247
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: USSN 08/144,992
; FILING DATE: 28-OCT-1993
; APPLICATION NUMBER: USSN 07/736,559
; FILING DATE: 26-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kempner, Ph.D., Gail M
; REGISTRATION NUMBER: 32,143
; REFERENCE/DOCKET NUMBER: REG 070C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; TELEX:
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-469-537A-85

Query Match          10.1%; Score 77; DB 2; Length 237;
Best Local Similarity 34.2%; Pred. No. 0.66;
Matches 27; Conservative 12; Mismatches 26; Indels 14; Gaps 4;

Qy 74 IADQVRLEQVMAGATNLQ-----MLMWCRLRELKDGPP--PSFLELMKVVIREEE---E 122
Db 118 LSNEQVLRFVMEGGLDKPDNCPDMLFELMRMCQYNPKMRPSFLELISSIKKEEMEGFR 177

Qy 123 EASF---ENESIEPBERD 138
Db 178 EVSFTYSEENKLPPEELD 196

RESULT 8
US-08-857-076-107
; Sequence 107, Application US/08857076C
; Patent No. 6225120
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Kimura, Routarou
; APPLICANT: Patterson, Garth
; APPLICANT: Ogg, Scott
; APPLICANT: Paradis, Suzanne
; APPLICANT: Tissenbaum, Heidi
; APPLICANT: Morris, Jason
```

```
; APPLICANT: Kowek, Allison
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: 00786/351001
; CURRENT APPLICATION NUMBER: US/08/857,076C
; CURRENT FILING DATE: 1997-05-15
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 107
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-857-076-107

Query Match      10.1%; Score 77; DB 3; Length 370;
Best Local Similarity 34.2%; Pred. No. 1.3;
Matches 27; Conservative 12; Mismatches 26; Indels 14; Gaps 4;

QY 74 IADQVRLEQVMAGATLQ-----MLWCRLRELKQGGP--PSFLELMKVIREEEE--E 122
Db 278 LSNEQVLRFVMEGLLKDPCDMLFELMRMCWQYNPKMRPSFLEIISIKKEEHPGPR 337

QY 123 EASF---ENESIEEPERD 138
Db 338 EVSFYSEENKLPPEELD 356

RESULT 9
US-09-107-532A-3677
; Sequence 3677, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSER: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3677:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
```

```
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...661
; SEQUENCE DESCRIPTION: SEQ ID NO: 3677:
US-09-107-532A-3677

Query Match      10.1%; Score 77; DB 4; Length 661;
Best Local Similarity 23.5%; Pred. No. 2.9;
Matches 31; Conservative 27; Mismatches 54; Indels 20; Gaps 4;

QY 9 DNPSSIVEECLFAFKQVFGSLESRTAQVRYLKPYQERGEKYSAYVLRLETLRLRAVEKR 68
Db 512 DVPEVSLVAILLADAKE--GFLRSERSLVQTIQRAARNEEGKVIMYADKVTDSMRLAMDET 569

QY 69 AIPRIADQVRLEQVMAGATLQMLWCRLRELKQGGPSPFLELMKVIREEEEEESPEN 128
Db 570 SRRRTIQKYNHEHGLIVKTI-----IKEIRD-----LISITKESEDDTKEAVQ 613

QY 129 ESIEE--PEERD 138
Db 614 VSYEEMTKEEKD 625

RESULT 10
US-08-249-687C-2
; Sequence 2, Application US/08249687C
; Patent No. 5942412
; GENERAL INFORMATION:
; APPLICANT: PRAGER, DIANE
; APPLICANT: MELMED, SHLOMO
; TITLE OF INVENTION: POLYNUCLEIC ACID ENCODING
; TITLE OF INVENTION: VARIANT INSULIN-LIKE GROWTH FACTOR I RECEPTOR BETA
; TITLE OF INVENTION: SUBUNIT & RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,687C
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/044,540
; FILING DATE: 06-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Basile, Lena
; REGISTRATION NUMBER: P-44,026
; REFERENCE/DOCKET NUMBER: P07 32349
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-622-7700
; TELEFAX: 213-489-4210
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1367 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-249-687C-2

Query Match      10.1%; Score 77; DB 2; Length 1367;
Best Local Similarity 34.2%; Pred. No. 8.1;
Matches 27; Conservative 12; Mismatches 26; Indels 14; Gaps 4;
```


[illegible]

```

RESULT 11
US-08-625-819-2
; Sequence 2, Application US/08625819
; Patent No. 5958872
; GENERAL INFORMATION:
; APPLICANT: O'CONNOR, Rosemary; and
; APPLICANT: BASERGA, Renato L.
; TITLE OF INVENTION: ACTIVE SURVIVAL DOMAINS OF IGF-IR
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
;

```

[illegible]

RESULT 12
US-08-746-559A-2
; Sequence 2, Application US/08746559A
; Patent No. 6084085
; GENERAL INFORMATION:
; APPLICANT: Renato Baserga
; APPLICANT: Mariana Resnicoff
; APPLICANT: Consuelo D'Ambrosio
; APPLICANT: Andre Ferber
; TITLE OF INVENTION: Method of In

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6084085
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/746,559A
FILING DATE: 13-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,699
FILING DATE: 14-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: TJU-2063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1367 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-746-559A-2

Query Match	10.1%;	Score 77;	DB 3;	Length 1367;
Best Local Similarity	34.2%;	Pred. No. 8.1;		
Matches 27;	Conservative 12;	Mismatches 26;	Indels	
Y	74	IADQVRLQVVMAGATLQ-----MLMCKRLRELKQGPP--PSFLMLMKV		
b	1216	LGNEQVRLFMVEGGLLDKPDNCDFMLFLMRCWQYNPKWRFSFLEIIS		
Y	123	EASF---ENESTEEPEERD 138		
b	1276	EVSFYYSSENKLPPEPEELD 1294		

```

RESULT 13
US-08-864-641B-18
; Sequence 18, Application US/08864641B
; Patent No. 6312684
; GENERAL INFORMATION:
; APPLICANT: Baserga, Renato
; APPLICANT: Abraham, David
; APPLICANT: Resnickoff, Mariana
; TITLE OF INVENTION: Method Of Inducing Resistance To Tumor Growth
; FILE REFERENCE: TJU2137
; CURRENT APPLICATION NUMBER: US/08/864,641B
; CURRENT FILING DATE: 1997-05-29
; PRIOR APPLICATION NUMBER: 08/340,732
; PRIOR FILING DATE: 1994-11-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 1367
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6312684el Sequence
US-08-864-641B-18

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RESULT 15
US-09-585-173B-51
Sovereign 51 Revolution US/09585173B

Search completed: September 27, 2004, 17:11:18
Job time : 9.54739 secs

Search completed: September 27, 2004, 17:11:18
Job time : 9.54739 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 17:02:20 ; Search time 25.0768 Seconds
(without alignments)
1678.826 Million cell updates/sec

Title: US-10-037-860-9

Perfect score: 766

Sequence: 1 DLHIVQADNPISVEGLE.....SIEPPEERDGYGRNHEGDD 149

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	766	100.0	149	3	AAB12527 Human Ma3
2	758	99.0	364	7	ADC08977 Onconeuro
3	755	98.6	283	3	AAB12528 Human Ma4
4	323	42.2	455	5	ABB05727 Human sig
5	323	42.2	463	3	AAB12529 Human Ma5
6	323	42.2	463	3	AAB42315 Human ORF
7	295.5	38.6	353	4	AAB74701 Human mem
8	287	37.5	452	6	AAO16179 Human pro
9	277	36.2	399	6	ADA54410 Human pro
10	277	36.2	399	6	ABG99947 Human nov
11	271.5	35.4	280	4	AAE01336 Human gen
12	271.5	35.4	351	4	AAE01340 Human gen
13	271.5	35.4	351	4	AAE01340 Human gen
14	271.5	35.4	351	4	AAU08664 Human mem
15	266.5	34.8	237	4	AAU08664 Human NOV
16	253.5	33.1	329	3	AB94854 Human pro
17	247.5	32.3	403	5	AB12525 Human pro
18	247.5	32.3	403	5	ABG97495 Human NOV
19	247.5	32.3	403	5	AAAS1624 Human pro
20	246.5	32.2	403	6	ABO14772 Novel hum
21	240	31.3	337	4	ABO14773 Novel hum
22	237	30.9	402	4	AAW25693 Human pro
23	225	29.4	312	3	AAAB60478 Human cel
24	180	23.5	80	4	AAAB43023 Human ORF
25	125	16.3	110	4	ABBI5036 Human ner
					AAO1787 Human pol

26 99.5 13.0 1270 6 ABO14659 Novel hum
27 98.5 12.9 525 5 ABB57353 Mouse isc
28 97.5 12.7 218 6 ADA55313 Human pro
29 97.5 12.7 543 4 AAM93466 Human pol
30 97.5 12.7 543 7 ADE57654 Human pro
31 96.5 12.6 541 7 ADE57652 Rat Prote
32 96.5 12.6 542 6 ABM04812 Rat NF-L
33 95.5 12.5 411 2 AAW24228 Human mel
34 94.5 12.3 475 2 AAW24228 Human mel
35 94.5 12.3 525 2 AAW24230 Human mel
36 90 11.7 592 5 ABG30418 Human tes
37 90 11.7 592 6 ABU00143 Human nov
38 89.5 11.7 563 2 AAW64228 Human sec
39 89.5 11.7 563 4 AAB90738 Human C22
40 89.5 11.7 760 5 ABB90912 Herbicida
41 89.5 11.7 760 7 ADB95024 A. thalia
42 89.5 11.7 800 2 AAW44003 A tumour
43 89.5 11.7 800 2 AAY27254 Human tum
44 89.5 11.7 800 4 AAB60503 Human cel
45 89.5 11.7 800 6 ABO53005 Human spl

ALIGNMENTS

RESULT 1
AAB12527

ID AAB12527 standard; protein; 149 AA.

XX AC AAB12527;

XX AC AAB12527;

DT 02-NOV-2000 (first entry)

XX Human Ma3 protein SEQ ID NO:9.

XX Ma1; Ma2; Ma3; Ma4; Ma5; paraneoplastic limbic encephalitis; diagnosis;
XX paraneoplastic syndrome; neoplasm; colon cancer; brainstem encephalitis;
XX breast cancer; parotid gland cancer; lung cancer; testicular cancer;
XX germ-cell tumour.

OS Homo sapiens.

XX JP2000146982-A.

XX 26-MAY-2000.

XX 10-NOV-1999; 99JP-00320171.

XX 10-NOV-1998; 98US-00189527.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX WPI; 2000-468119/41.

XX N-PSDB; AAA60835.

PT Diagnosing paraneoplastic syndrome e.g. paraneoplastic limbic
PT encephalitis or neoplasm e.g. colon cancer comprising assessing a test
PT sample for the presence or absence of antibodies to a Ma family
PT polypeptide.

XX Claim 48; Fig 6; 27pp; Japanese.

CC The present invention describes a method for diagnosing a paraneoplastic
CC syndrome or neoplasm. The method comprises assessing a test sample for
CC the presence or absence of antibodies to a Ma family polypeptide (I). The
CC method is used to diagnose a paraneoplastic syndrome especially
CC paraneoplastic limbic encephalitis and/or brainstem encephalitis or
CC neoplasm in an individual. The method diagnoses the neoplasm by assessing
CC antibodies to (I) preferably Ma1, which is indicative presence of breast
CC cancer, colon cancer, parotid gland cancer, lung cancer, testicular
CC cancer and germ-cell tumours of Ma2, which is indicative of testicular
CC cancer, germ-cell tumour, and lung cancer. The present sequence is the
CC Ma3 protein as given in the present invention

```
XX SQ Sequence 149 AA;
Query Match 100.0%; Score 766; DB 3; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.8e-75;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRLKPYQEGEKVSAYVLRLETL 60
Db 1 DLHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRLKPYQEGEKVSAYVLRLETL 60
QY 61 LRRAVEKAIARRIADQVRLQVWAGATLNQMLWCLRELKQDQPPSPFLELMKVIREEE 120
Db 61 LRRAVEKAIARRIADQVRLQVWAGATLNQMLWCLRELKQDQPPSPFLELMKVIREEE 120
QY 121 EEEASFENESIEEPEERDGYGRWNHEGDD 149
Db 121 EEEASFENESIEEPEERDGYGRWNHEGDD 149

RESULT 2
ADC08977
ID ADC08977 standard; protein; 364 AA.
XX
AC ADC08977;
XX
DT 18-DEC-2003 (first entry)
XX
DE Onconeural antigen Ma2 protein.
XX
KW Human; Ma2; onconeural; antigen; Alzheimer's disease;
KW neurodegenerative disease; diagnosis; neuroprotective; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003073104-A2.
XX
PD 04-SEP-2003.
XX
PF 26-FEB-2003; 2003WO-BP001946.
XX
PR 26-FEB-2002; 2002EP-00004177.
PR 26-FEB-2002; 2002US-0359307P.
XX
PA (EVOT-) EVOTEC NEUROSCIENCES GMBH.
XX
PI Hipfel R, Von Der Kammer H, Pohlner J;
XX
PP WPI; 2003-721818/68.
XX
DR GENBANK; O94959, KIA00883.
XX
PT Diagnosing or prognosticating, or determining increased risk of
PT developing a neurodegenerative disease by determining level or activity
PT of a transcription or translation product of a gene coding for Ma
PT onconeural antigen.
XX
PS Disclosure; Fig 9; 51pp; English.
XX
XX The present sequence is the protein sequence of human onconeural
XX antigen Ma2. The invention discloses the detection and differential
XX expression and regulation of the Ma2 gene in specific brain regions of AD
XX patients. The Ma2 gene and its transcription and/or translation products
XX may have a causative role in the regional selective neuronal degeneration
XX typically observed in AD, or may confer a neuroprotective function to the
XX remaining nerve cells. Methods are claimed for diagnosing or
XX prognosticating a neurodegenerative disease, for monitoring the
XX progression of a neurodegenerative disease, and for evaluating treatment
XX of a neurodegenerative disease, especially AD, in a subject by
XX determining the level and/or activity of a transcription or translation
XX product of an Ma onconeural antigen gene, especially Ma2. Also claimed
XX are: a method for treating or preventing AD and related neurodegenerative
XX disorders using the Ma2 gene or its transcription or translation product;
XX a method of screening for modulating agents of neurodegenerative diseases
```

```
CC ; and a recombinant non-human animal comprising an Ma2 gene sequence,
CC which is useful for screening, testing and validating candidate
CC diagnostic and therapeutic agents.
XX
SQ Sequence 364 AA;
Query Match 99.0%; Score 758; DB 7; Length 364;
Best Local Similarity 99.3%; Pred. No. 4.4e-74;
Matches 148; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DLHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRLKPYQEGEKVSAYVLRLETL 60
Db 216 DLHIVQADNPSISVEECLEAFKQVFGSLESRRTAQVRLKPYQEGEKVSAYVLRLETL 275
QY 61 LRRAVEKAIARRIADQVRLQVWAGATLNQMLWCLRELKQDQPPSPFLELMKVIREEE 120
Db 276 LRRAVEKAIARRIADQVRLQVWAGATLNQMLWCLRELKQDQPPSPFLELMKVIREEE 335
QY 121 EEEASFENESIEEPEERDGYGRWNHEGDD 149
Db 336 EEEASFENESIEEPEERDGYGRWNHEGDD 364

RESULT 3
AAB12528
ID AAB12528 standard; protein; 283 AA.
XX
AC AAB12528;
XX
DT 02-NOV-2000 (first entry)
XX
DE Human Ma4 protein SEQ ID NO:11.
XX
KW Ma1; Ma2; Ma3; Ma4; Ma5; paraneoplastic limbic encephalitis; diagnosis;
KW paraneoplastic syndrome; neoplasm; colon cancer; brainstem encephalitis;
KW breast cancer; parotid gland cancer; lung cancer; testicular cancer;
KW germ-cell tumour.
XX
OS Homo sapiens.
XX
PN JP2000146982-A.
XX
PD 26-MAY-2000.
XX
PF 10-NOV-1999; 99JP-00320171.
XX
PR 10-NOV-1998; 98US-00189527.
XX
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
PP WPI; 2000-468119/41.
XX
DR N-PSDB; AAM60836.
XX
PT Diagnosing paraneoplastic syndrome e.g. paraneoplastic limbic
PT encephalitis or neoplasm e.g. colon cancer comprising assessing a test
PT sample for the presence or absence of antibodies to a Ma family
PT polypeptide.
XX
PS Claim 48; Fig 7-8; 27pp; Japanese.
XX
XX The present invention describes a method for diagnosing a paraneoplastic
XX syndrome or neoplasm. The method comprises assessing a test sample for
XX the presence or absence of antibodies to a Ma family polypeptide (I). The
XX method is used to diagnose a paraneoplastic syndrome especially
XX paraneoplastic limbic encephalitis and/or brainstem encephalitis or
XX neoplasm in an individual. The method diagnoses the neoplasm by assessing
XX antibodies to (I) preferably Ma1, which is indicative presence of breast
XX cancer, colon cancer, parotid gland cancer, lung cancer, testicular
XX cancer and germ-cell tumour or Ma2, which is indicative of testicular
XX cancer, germ-cell tumour, and lung cancer. The present sequence is the
XX Ma4 protein as given in the present invention
XX
SQ Sequence 283 AA;
```

Query Match	98.6%;	Score 755;	DB 3;	Length 283;
Best Local Similarity	98.7%;	Pred. No. 6.7e-74;		
Matches 147;	Conservative	1;	Mismatches	1; Indels 0; Gaps 0;
QY	1	DLMHVQADNP	PSIVEECLAEAFKQVFGSLESRRTAQVRLKPVQEBEGKVSAYVLRLETL	60
Db	135	DLMHVQADNP	PSIVEECLAEAFKQVFGSLESRRTAQVRLKPVQEBEGKVSAYVLRLETL	194
QY	61	LRAVEKRAIP	RIADQVRLQVLEQVMAGATLNQMLWCRLEKLDQGGPPPSFLELMKVIREEE	120
Db	195	LRAVEKRAIP	RIADQVRLQVLEQVMAGATLNQMLWCRLEKLDQGGPPPSFLELMKVIREEE	254
QY	121	BEEASFENES	IEPERDQYGRWNHEGDD	149
Db	255	BEEASFENES	IEPERDQYGRWNHEGDD	283
RESULT 4				
ID	ABB05727	standard; protein; 455 AA.		
XX				
AC	ABB05727;			
XX				
DT	30-APR-2002	(first entry)		
XX				
DE		Human signal transduction protein clone tes3_5k22.		
XX				
KW		Human; foetal brain; foetal kidney; melanoma; testis; amygdala;		
KW		gene therapy.		
XX				
OS		Homo sapiens.		
XX				
PN	WO200198454-A2.			
XX				
PD	27-DEC-2001.			
XX				
PF	25-APR-2001; 2001WO-IB002050.			
XX				
PR	25-APR-2000; 2000US-0199380P.			
XX				
PA	(GEHU-) GERMAN HUMAN GENOME PROJECT.			
XX				
PI	Wiemann S;			
XX				
DR	WPI; 2002-055860/07.			
XX	N-PSDB; ABA93764.			
XX				
PT	Human cDNA sequences and clones derived from human fetal brain, fetal			
PT	kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic			
PT	screening and therapy.			
XX				
PS	Claim 1; Page 382; 61pp; English.			
XX				
CC	The present invention describes assemblages and computer readable media			
CC	comprising novel human cDNA sequences and clones derived from human			
CC	foetal brain, foetal kidney, melanoma, testis and amygdala cDNA			
CC	libraries. ABA93702 to ABA93766 represent human cDNA sequences from the			
CC	present invention which encode the proteins given in ABB05662 to			
CC	ABB05729. The human cDNA sequences and clones can be used in gene			
CC	therapy. The clones may be used in a variety of applications, for example			
CC	they may be used in profiling assays, for providing large arrays of human			
CC	genetic material for implementing large-scale screening strategies and			
CC	for treating diseases via gene therapy procedures			
XX				
SQ	Sequence 455 AA;			
Query Match	42.2%;	Score 323;	DB 5;	Length 455;
Best Local Similarity	52.7%;	Pred. No. 2.1e-26;		
Matches 68;	Conservative	26;	Mismatches	33; Indels 2; Gaps 1;
QY	6	VQADNP	PSIVEECLAEAFKQVFGSLESRRTAQVRLKPVQEBEGKVSAYVLRLETL	65
Db	135	VQADNP	PSIVEECLAEAFKQVFGSLESRRTAQVRLKPVQEBEGKVSAYVLRLETL	194
QY	61	LRAVEKRAIP	RIADQVRLQVLEQVMAGATLNQMLWCRLEKLDQGGPPPSFLELMKVIREEE	120
Db	195	LRAVEKRAIP	RIADQVRLQVLEQVMAGATLNQMLWCRLEKLDQGGPPPSFLELMKVIREEE	254
QY	121	BEEASFENES	IEPERDQYGRWNHEGDD	149
Db	255	BEEASFENES	IEPERDQYGRWNHEGDD	283
RESULT 5				
AAB12529				
ID	AAB12529	standard; protein; 463 AA.		
XX				
AC	AAB12529;			
XX				
DT	02-NOV-2000	(first entry)		
XX				
DE		Human Ma5 protein SEQ ID NO:13.		
XX				
KW		Ma1; Ma3; Ma4; Ma5; paraneoplastic limbic encephalitis; diagnosis;		
KW		paraneoplastic syndrome; neoplasm; colon cancer; brainstem encephalitis;		
KW		breast cancer; parotid gland cancer; lung cancer; testicular cancer;		
KW		germ-cell tumour.		
XX				
OS		Homo sapiens.		
XX				
PN	JP2000146982-A.			
XX				
PD	26-MAY-2000.			
XX				
PF	10-NOV-1999; 99JP-00320171.			
XX				
PR	10-NOV-1998; 98US-00189527.			
XX				
PA	(SLOK) SLOAN KETTERING INST CANCER RES.			
XX				
DR	WPI; 2000-468119/41.			
XX	N-PSDB; AAA60837.			
XX				
PT	Diagnosing paraneoplastic syndrome e.g. paraneoplastic limbic			
PT	encephalitis or neoplasm e.g. colon cancer comprising assessing a test			
PT	sample for the presence or absence of antibodies to a Ma family			
PT	polypeptide.			
XX				
PS	Claim 48; Fig 9-10; 27pp; Japanese.			
XX				
CC	The present invention describes a method for diagnosing a paraneoplastic			
CC	syndrome or neoplasm. The method comprises assessing a test sample for			
CC	the presence or absence of antibodies to a Ma family polypeptide (I). The			
CC	method is used to diagnose a paraneoplastic syndrome especially			
CC	paraneoplastic limbic encephalitis and/or brainstem encephalitis or			
CC	neoplasm in an individual. The method diagnoses the neoplasm by assessing			
CC	antibodies to (I) preferably Ma1, which is indicative presence of breast			
CC	cancer, colon cancer, parotid gland cancer, lung cancer, testicular			
CC	cancer and germ-cell tumours or Ma2, which is indicative of testicular			
CC	cancer, germ-cell tumour, and lung cancer. The present sequence is the			
CC	Ma5 protein as given in the present invention			
XX				
SQ	Sequence 463 AA;			
Query Match	42.2%;	Score 323;	DB 3;	Length 463;
Best Local Similarity	52.7%;	Pred. No. 2.1e-26;		
Matches 68;	Conservative	26;	Mismatches	33; Indels 2; Gaps 1;
QY	6	VOADNP	PSIVEECLAEAFKQVFGSLESRRTAQVRLKPVQEBEGKVSAYVLRLETL	65
Db	135	VOADNP	PSIVEECLAEAFKQVFGSLESRRTAQVRLKPVQEBEGKVSAYVLRLETL	194
QY	66	EKRAIP	RIADQVRLQVLEQVMAGATLNQMLWCRLEKLDQGGPPPSFLELMKVIREEE	125
Db	280	ENNVSRRNVN	QTLKRVLSGATLPDKLRDKLKMQRKPPGFLALVKLLREEEWEAT	339

CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, anti-inflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive

XX
SQ Sequence 463 AA;

Query Match 42.2%; Score 323; DB 3; Length 463;
Best Local Similarity 52.7%; Pred. No. 2.le-26;
Matches 68; Conservative 26; Mismatches 33; Indels 2; Gaps 1;

Qy 6 VQADNPSISVERCLEAFKOVGSLRRRTAQRVYLKPQEKGKVSAVLLETLRRAV 65
: : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 220 LRASNASITVEECLAAQQVFGEVSHKIAQVKLKCAVQAGEKVSSFLPLELQRAV 279

Qy 66 EKRAIPRIADQVRLEQVMAGATLNQMLWCRILRELKDQPPSPFLELMKVIREEEEBAS 125
: : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 280 ENNVSRNRVNQTRLKRVLSGATLPDKLRDLKMKQRKKPGPLVALVKLLRESEWEAT 339

Qy 126 F--ENESIE 132
: | | |
Db 340 LGPDRESLE 348

RESULT 7
AAB74701
ID AAB74701 standard; protein; 353 AA.
AC AAB74701;
XX
DT 12-JUN-2001 (first entry)
DE XX
XX Human membrane associated protein MEMAP-7.
KW Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrheic;
KW antiarteriosclerotic; gene therapy; cell proliferative disorder;
KW autoimmune disorder; inflammatory disorder; neurological disorder;
KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;
KW epilepsy; diarrhoea.
XX
OS Homo sapiens.
XX WO200112662-A2.
PN
PD 22-FEB-2001.
XX
PF 14-AUG-2000; 2000WO-US022315.
XX
PR 17-AUG-1999; 99US-0149641P.
PR 09-NOV-1999; 99US-0164203P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;
PI Baughn MR, Lu DAM, Patterson C;
XX WPI; 2001-168860/17.
DR N-PSDB; AAF81747.
XX Isolated polypeptide with a human membrane associated protein sequence is useful for the diagnosis, prevention and treatment of cell proliferative, autoimmune/inflammatory, neurological and gastrointestinal disorders.

Claim 1; Page 119-120; 173pp; English.

AAF81741 to AAF81777 encode the human membrane associated proteins (MEMAP) given in AAB74695 to AAB74731. MEMAPS have cytostatic, antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic and antiarteriosclerotic activities, which can be used in gene therapy. CC MEMAPS and agonist of MEMAPS can be used to treat a disease or condition associated with decreased expression of functional MEMAP and antagonists of MEMAP are used to treat a disease or condition associated with

CC overexpression of functional MEMAP. These disorders include cell
 CC proliferative, autoimmune/inflammatory, neurological and gastrointestinal
 CC disorders. The MEMAP polynucleotides and proteins are also used for the
 CC diagnosis of these disorders. Specific examples of these disorders
 CC include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
 CC MEMAP proteins can be used to screen for compounds which specifically
 CC bind MEMAP including antibodies, oligonucleotides, proteins and small
 CC molecules. MEMAP polynucleotides can be used to prepare transgenic
 CC animals which can be studied to provide information concerning human
 CC disease. Anti-MEMAP antibodies are useful in immunoassays for the
 CC detection of MEMAP protein and can be used as antagonists to treat or
 CC prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
 CC can be delivered to target cells with genetic abnormalities with respect
 CC to the expression of MEMAP to treat or prevent a disorder associated with
 CC MEMAP

XX Sequence 353 AA;
 SQ
 Query Match 38.6%; Score 295.5; DB 4; Length 353;
 Best Local Similarity 46.3%; Pred. No. 1.5e-23;
 Matches 62; Conservative 29; Mismatches 36; Indels 7; Gaps 2;
 QY 1 DLMHIVQADNPISVVEECLEAFKQVFGSLESRRTAQVRYLKPQBEQEKVSAYVLRLETL 60
 Db 212 DVIRILKSNPAITTAECLEKALEQVFGSVSSRDQIKFLNTYQNPGEKLSAYVIRLEPL 271
 QY 61 LRRAVEKRAIPRRIADQVRLEQVMAGA-----TLNQMLWCRLRELKDQGPSPFLELMKVI 116
 Db 272 LQKVEKGAIDKQNVQARLEQVITAGANHSQAIRQLWL---TGAGEGAPNLFQILLVQI 328
 QY 117 REEEEEEASFENES 130
 Db 329 REBEAKEEEEEEAEA 342

RESULT 8
 AAOL16179
 ID AAO16179 standard; protein; 452 AA.
 AC AAO16179;
 DT 28-MAR-2003 (first entry)
 DE Human protein #5.
 XX Human; vaccine; adult whole brain; foetal whole brain; tonsil;
 KW adult hippocampus; disease-associated SNP analysis; knockout mouse;
 KW disease model mouse; cancer; neurological disorder.
 XX
 OS Homo sapiens.
 XX WO200299103-A1.
 PN 12-DEC-2002.
 PD
 XX 27-MAY-2002; 2002WO-JP005134.
 XX
 PR 04-JUN-2001; 2001JP-00168370.
 PR 16-AUG-2001; 2001JP-00246915.
 XX
 XX (KAZU-) KAZUSA DNA RES INST FOUND.
 PA (PROT-) PROTEIN EXPRESS CO LTD.
 XX
 XX Ohara O, Nagase T, Nakajima D;
 PI
 XX WPI; 2003-140622/13.
 DR N-PSDB; AAL51207.
 XX
 XX DNA preferentially expressed in human adult and fetal brain tissue useful
 PT for diagnosis, treatment and analysis of cancer and mental disorders.
 PT
 XX
 PS Claim 1; Page 56-60; 73pp; Japanese.

CC The invention comprises the amino acid and coding sequences of seven
 CC human proteins that are preferentially expressed in adult whole brain,
 CC foetal whole brain, tonsil and adult hippocampus tissue. The DNA
 CC sequences are useful for the analysis of disease-associated single
 CC nucleotide polymorphisms and the production of knockout and human disease
 CC model mice. The DNA and protein sequences of the invention are useful for
 CC the prevention (vaccine) and treatment of cancer and neurological
 CC disorders. The present amino acid sequence represents a human protein of
 CC the invention
 XX
 SQ Sequence 452 AA;

Query Match 37.5%; Score 287; DB 6; Length 452;
 Best Local Similarity 43.8%; Pred. No. 1.8e-22;
 Matches 63; Conservative 30; Mismatches 43; Indels 8; Gaps 2;
 QY 2 LMHVQADNPISVVEECLEAFKQVFGSLESRRTAQVRYLKPQBEQEKVSAYVLRLETL 61
 Db 215 IMRVQANDSITVEQCCLDAKQIFGDKEDFRASQFRPLQTSKIGEKVSTFLRLEPL 274
 QY 62 RRAVEKRAIPRRIADQVRLEQVMAGATLNQMLWCRLRELKDQGPSPFLELMKVIREEE 121
 Db 275 QKAVHKSPLSVSRSTDMIRLKHLLARVAMTPALRGKLELLDQRCPPNPFLELMKLRDEE 334
 QY 122 ---EEASFENESIEEPEERDGYGR 142
 Db 335 WENTEAVMNK-----EKPSGRGR 353

RESULT 9
 ADA54410
 ID ADA54410 standard; protein; 399 AA.
 XX ADA54410;
 XX
 DT 20-NOV-2003 (first entry)
 DE Human protein, SEQ ID 1978.
 XX
 KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
 KW inflammatory disease; osteoporosis; neurological disease.
 XX
 OS Homo sapiens.
 XX EP1293569-A2.
 PN 19-MAR-2003.
 PD
 XX 21-MAR-2002; 2002EP-00006586.
 PF
 XX 14-SEP-2001; 2001JP-00328381.
 PR 24-JAN-2002; 2002US-0350435P.
 XX
 XX (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX
 DR WPI; 2003-395539/38.
 DR N-PSDB; ADA52771.
 XX
 XX New polynucleotides encoding full-length polypeptides, e.g. secretory
 PT and/or membrane proteins, useful for developing medicines for diseases in
 PT which the gene is involved, or as target molecules for gene therapy.
 XX
 PS Claim 14; SEQ ID NO 1978; 205pp; English.
 XX
 CC The present invention relates to novel human secretory or membrane
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
 CC ADA54071). The coding sequences are useful in the gene therapy of

disorders, osteoporosis, osteoarthritis, bone degenerative disorders, periodontal disease, liver fibrosis, infections (e.g. viral, fungal or bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis). Sequences ABG9988-ABG9989 and ABU0010-ABU00433 represent human polypeptides of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied by the European Patent Office

Query Match 36.2%; Score 277; DB 6; Length 399;
Best Local Similarity 43.5%; Pred. No. 1.9e-21;
Matches 60; Conservative 30; Mismatches 48; Indels 0; Gaps 0;

2 LMHVQADNPISVVECEAFKQVFGSLESRRTAQVRLKPYQEGEKVSAYVLRLETL 61
208 LVHALLAENPARTAQDCLLAALQVFGDNESQATIRVKCLTAQQQSGERLSAFVLRLEVL 267

62 RRAVEKRAIPRIADQVRLQVMAQATNQMLWCRLKDGQPPPSFLEMLKVIREEE 121
268 QKAMEKEALASADRVLRQMLTRAHLTEPLDEALRKLRMAGRSFLEMLGLVRESEA 327

122 EASFENESIEPBERDG 139
328 WEASLARSVRAQTQEGAG 345

RESULT 11
ID AAE01336 standard; protein; 280 AA.
XX AAE01336;
XX 17-JUL-2001 (first entry)
XX Human gene 22 encoded secreted protein fragment, SEQ ID NO:201.
XX Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiotensin-related disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; infection; wound healing; vulvar; cell culture;
KW chemotaxis; food additive; gene therapy; binding partner identification.
XX Homo sapiens.
XX OS
XX WO200134769-A2.
XX 17-MAY-2001.
XX 01-NOV-2000; 2000WO-US030040.
XX 05-NOV-1999; 99US-0163580P.
XX 30-JUN-2000; 2000US-0215130P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Komatsoulis GA, Wei P, Baker KP, Fiscella M;
XX WPI; 2001-308781/32.
XX New isolated nucleic acid molecule encoding a human secreted protein is
PT used in preventing, treating or ameliorating a medical condition.
XX Disclosure; Page 46; 519pp; English.
PS
XX AAD05121-AA05203 represent cDNAs corresponding to 24 human secreted
CC protein genes, and AAE01232-AAE01311 represent the proteins they encode.
CC AAE01312-AAE01340 represent human secreted protein variants or fragments.

diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.

Query Match 36.2%; Score 277; DB 6; Length 399;
Best Local Similarity 43.5%; Pred. No. 1.9e-21;
Matches 60; Conservative 30; Mismatches 48; Indels 0; Gaps 0;

2 LMHVQADNPISVVECEAFKQVFGSLESRRTAQVRLKPYQEGEKVSAYVLRLETL 61
208 LVHALLAENPARTAQDCLLAALQVFGDNESQATIRVKCLTAQQQSGERLSAFVLRLEVL 267

62 RRAVEKRAIPRIADQVRLQVMAQATNQMLWCRLKDGQPPPSFLEMLKVIREEE 121
268 QKAMEKEALASADRVLRQMLTRAHLTEPLDEALRKLRMAGRSFLEMLGLVRESEA 327

122 EASFENESIEPBERDG 139
328 WEASLARSVRAQTQEGAG 345

RESULT 10
ID ABG99947 standard; protein; 399 AA.
XX ABG99947;
XX 17-JAN-2003 (first entry)
XX Human novel polypeptide #60.
XX Human; genetic disorder; gene mapping; medical imaging; cancer;
KW neurodegenerative disorder; lymphoid cell disorder; osteoporosis;
KW Parkinson's disease; Alzheimer's disease; bone degenerative disorder;
KW osteoarthritis; periodontal disease; liver fibrosis; viral infection;
KW fungal infection; bacterial infection; autoimmune disease; diabetes;
KW atopic dermatitis.
XX Homo sapiens.
XX OS
XX WO200274961-A1.
XX 26-SEP-2002.
XX 14-MAR-2002; 2002WO-US005109.
XX 15-MAR-2001; 2001US-00810173.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Zhou P, Goodrich R, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX WPI; 2003-040556/03.
XX N-PSDB; ABX05045.
XX New isolated polypeptides and polynucleotides, useful for preventing,
PT treating or ameliorating medical conditions, such as cancer,
PT neurodegenerative disorders, lymphoid cell disorders, bone degenerative
PT disorders, and infections.
XX Claim 9; SEQ ID NO 586; 235pp; English.
XX The invention relates to human polynucleotides and the polypeptides they
CC encode. The polynucleotides and polypeptides are useful in diagnostics,
CC forensics, gene mapping, medical imaging, identification of mutations
CC responsible for genetic disorders or other traits, assessing biodiversity
CC and producing many other types of data and products dependent on DNA and
CC amino acid sequences. They are also useful for preventing, treating or
CC ameliorating medical conditions, such as cancer, neurodegenerative
CC disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell

CC The secreted proteins and their genes are useful for preventing, treating
 CC or ameliorating medical conditions, e.g., by protein or gene therapy.
 CC Pathological conditions can be diagnosed by determining the amount of the
 CC new protein in a sample or by determining the presence of mutations in
 CC the new genes. Specific uses are described for each of the 24 genes,
 CC based on the tissues in which they are most highly expressed, and include
 CC developing products for the diagnosis or treatment of proliferative
 CC disorders, cancer, tumors, foetal and developmental abnormalities,
 CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
 CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
 CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
 CC pregnancy-related disorders, endocrine disorders, and infections. The
 CC proteins can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues, to identify their cognate ligands or binding
 CC partners, and in chemotaxis, and can be used as a food additive or
 CC preservative to modify storage properties. Antibodies specific for a
 CC protein of the invention can be used in alleviating symptoms associated
 CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
 CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
 CC present sequence represents a human secreted protein fragment referred to
 CC in the disclosure of the invention
 CC
 CC SQ Sequence 280 AA;

Query Match 35.4%; Score 271.5; DB 4; Length 280;
 Best Local Similarity 44.6%; Pred. No. 4.7e-21;
 Matches 58; Conservative 32; Mismatches 29; Indels 11; Gaps 3;

QY 1 DLMHIVQADNPSTVBECELEAFQVFGSLERSTAQVRYLKPQBEKVSAYVLETL 60
 Db 145 DVIRVLKINNPILTVECLQALEEVFGVDNPRELQVKYLTYYQKDEKLSAYVLEPL 204
 QY 61 LRAVEKRAIPRIADQVRLEQVMAGA---TLNQMLWCLRELKDGQPPSPFLELMKVIR 117
 Db 205 LQKLVQGAERDAVQARLDQVIAGAVHKTIRREL-----NLPEDGAPGFLQLLVLIK 259
 QY 118 E---EEEEEA 124
 Db 260 DYEAEEEEEA 269

RESULT 12

AAE01340
 ID AAE01340 standard; protein; 351 AA.

XX AAE01340;

XX 17-JUL-2001 (first entry)

XX Human gene 22 encoded secreted protein fragment, SEQ ID NO:205.

XX Human; secreted protein; proliferative disorder; cancer; tumour;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder;
 KW endocrine disorder; infection; wound healing; vulnerability; cell culture;
 KW chemotaxis; food additive; gene therapy; binding partner identification.

XX Homo sapiens.

XX WO200134769-A2.

XX 17-MAY-2001.

XX

PF 01-NOV-2000; 2000MO-US030040.

XX 05-NOV-1999; 99US-0163580P.

PR 30-JUN-2000; 2000US-0215130P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Ruben SM, Komatsoulis GA, Wei P, Baker KP, Fiscella M;

XX WPI; 2001-308781/32.

DR New isolated nucleic acid molecule encoding a human secreted protein is

XX used in preventing, treating or ameliorating a medical condition.

PT Disclosure; Page 46; 519pp; English.

XX AAD05121-AAD05203 represent cDNAs corresponding to 24 human secreted

XX protein genes, and AAE0132-AAE01311 represent the proteins they encode.

CC The secreted proteins and their genes are useful for preventing, treating

CC or ameliorating medical conditions, e.g., by protein or gene therapy.

CC Pathological conditions can be diagnosed by determining the amount of the

CC new protein in a sample or by determining the presence of mutations in

CC the new genes. Specific uses are described for each of the 24 genes,

CC based on the tissues in which they are most highly expressed, and include

CC developing products for the diagnosis or treatment of proliferative

CC disorders, cancer, tumors, foetal and developmental abnormalities,

CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,

CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),

CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,

CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,

CC angiogenic disorders, kidney disorders, gastrointestinal disorders,

CC pregnancy-related disorders, endocrine disorders, and infections. The

CC proteins can also be used to aid wound healing and epithelial cell

CC proliferation, to prevent skin aging due to sunburn, to maintain organs

CC before transplantation, for supporting cell culture of primary tissues,

CC to regenerate tissues, to identify their cognate ligands or binding

CC partners, and in chemotaxis, and can be used as a food additive or

CC preservative to modify storage properties. Antibodies specific for a

CC protein of the invention can be used in alleviating symptoms associated

CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,

CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The

CC present sequence represents a human secreted protein fragment referred to

CC in the disclosure of the invention
 CC
 CC SQ Sequence 351 AA;

Query Match 35.4%; Score 271.5; DB 4; Length 351;

Best Local Similarity 44.6%; Pred. No. 6.4e-21;

Matches 58; Conservative 32; Mismatches 29; Indels 11; Gaps 3;

QY 1 DLMHIVQADNPSTVBECELEAFQVFGSLERSTAQVRYLKPQBEKVSAYVLETL 60

Db 216 DVIRVLKINNPILTVECLQALEEVFGVDNPRELQVKYLTYYQKDEKLSAYVLEPL 275

QY 61 LRAVEKRAIPRIADQVRLEQVMAGA---TLNQMLWCLRELKDGQPPSPFLELMKVIR 117

Db 276 LQKLVQGAERDAVQARLDQVIAGAVHKTIRREL-----NLPEDGAPGFLQLLVLIK 330

QY 118 E---EEEEEA 124

Db 331 DYEAEEEEEA 340

RESULT 13

AAE01340

ID AAE01340 standard; protein; 351 AA.

XX AAE01340;

XX 12-JUN-2001 (first entry)

XX

DE Human membrane associated protein MEMAP-1.
XX Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrhetic;
KW antiarteriosclerotic; gene therapy; cell proliferative disorder;
KW autoimmune disorder; inflammatory disorder; neurological disorder;
KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;
KW epilepsy; diarrhoea.
XX Homo sapiens.
XX WO200112662-A2.
XX 22-FEB-2001.
XX 14-AUG-2000; 2000WO-US022315.
XX 17-AUG-1999; 99US-0149641P.
XX 09-NOV-1999; 99US-0164203P.
XX (INCY-) INCYTE GENOMICS INC.
XX Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;
PI Baughn MR, Lu DAM, Patterson C;
XX WPI; 2001-168860/17.
XX N-PSDB; AAF81741.
XX Isolated polypeptide with a human membrane associated protein sequence is
XX useful for the diagnosis, prevention and treatment of cell proliferative,
XX autoimmune/inflammatory, neurological and gastrointestinal disorders.
XX Claim 1; Page 114-115; 173pp; English.
XX AAF81741 to AAF81777 encode the human membrane associated proteins
XX (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,
XX antiinflammatory, anticonvulsant, immunosuppressive, antidiarrhetic and
XX antiarteriosclerotic activities, which can be used in gene therapy.
XX MEMAPs and agonist of MEMAPs can be used to treat a disease or condition
XX associated with decreased expression of functional MEMAP and antagonists
XX of MEMAP are used to treat a disease or condition associated with
XX overexpression of functional MEMAP. These disorders include cell
XX proliferative, autoimmune/inflammatory, neurological and gastrointestinal
XX disorders. The MEMAP polynucleotides and proteins are also used for the
XX diagnosis of these disorders. Specific examples of these disorders
XX include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
XX MEMAP proteins can be used to screen for compounds which specifically
XX bind MEMAP including antibodies, oligonucleotides, proteins and small
XX molecules. MEMAP polynucleotides can be used to prepare transgenic
XX animals which can be studied to provide information concerning human
XX disease. Anti-MEMAP antibodies are useful in immunoassays for the
XX detection of MEMAP protein and can be used as antagonists to treat or
XX prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
XX can be delivered to target cells with genetic abnormalities with respect
XX to the expression of MEMAP to treat or prevent a disorder associated with
XX MEMAP
XX SQ Sequence 351 AA;
Best Match 35.4%; Score 271.5; DB 4; Length 351;
Query Local Similarity 44.6%; Pred. No. 6.4e-21;
Matches 58; Conservative 33; Mismatches 29; Indels 11; Gaps 3;
QY 1 DLMHIVQADNPSTVSECLAFQVKGSLRSTQVRLKPYQEGEKVSAVLETL 60
DB 216 DVIRVLKINPLITVDECLQALBEVFGVTDPNRELQVKYLTYYKDEEKL SAVLLEPL 275
QY 61 LRFAVEKRAIPRIADQVRLQVWAGA---TLNQLWCLRELKDGQPPSFLELMKVIR 117
DB 276 LQKLVGALIERDAVQARLDQVAGVHTIRREL-----NLPEDGAPGFFQLLVLIK 330
QY 118 E---EEEEEA 124
;

Db 331 DYEAABEEEA 340
RESULT 14
AAU08664
ID AAU08664 standard; protein; 351 AA.
XX AC AAU08664;
XX 18-DEC-2001 (first entry)
XX Human NOV8 protein.
XX Human; NOV8; cytostatic; nootropic; neuroprotective; vulvarary;
KW cerebroprotective; antiparkinsonian; hypotensive; antiasthmatic;
KW antidiabetic; antipsoriatic; antiinflammatory; immunosuppressive;
KW antiatherosclerotic; dermatological; cancer; neurological disorder;
KW Parkinson's disease; diabetes mellitus; asthma; enamel defect;
KW immune disorder; autoimmune disease; respiratory disorder; bone disorder;
KW musculoskeletal disorders; leukaemia; lymphoma;
KW cell growth regulation disorder; lesional psoriatic skin;
KW atherosclerosis; abdominal aortic aneurysm.
XX Homo sapiens.
XX WO200168851-A2.
XX 20-SEP-2001.
XX 12-MAR-2001; 2001WO-US007735.
XX 10-MAR-2000; 2000US-0188277P.
XX 10-MAR-2000; 2000US-0188316P.
XX 14-MAR-2000; 2000US-0189139P.
XX 14-MAR-2000; 2000US-0189140P.
XX 17-MAR-2000; 2000US-0190231P.
XX 17-MAR-2000; 2000US-0190401P.
XX (CURA-) CURAGEN CORP.
XX Padigar M, Vernet CAM, Fernandes E, Shimkets RA, Spaderna SK;
PI Majumder K, Li L;
XX WPI; 2001-570869/64.
XX N-PSDB; AAS13342.
XX Novel polypeptides and nucleic acids homologous to members of collagen,
XX potassium channel, tuftelin family of proteins for diagnosing, treating
XX cancer, atherosclerosis, neurological, skin and enamel defect disorders.
XX Claim 1; Page 29; 128pp; English.
XX The invention relates to isolated NOVX (NOVX1-11) polypeptides and the
XX polynucleotides that encode them. NOVX polypeptides, polynucleotides and
XX anti-NOVX antibodies are useful for treating or preventing a pathology
XX associated with NOVX polypeptide in humans and for treating a syndrome
XX associated with human disease e.g. disorders characterised by altered
XX cell motility, proliferation and migration e.g. cancer, angiogenesis and
XX wound healing (NOV1-3), neurological disorders, e.g. episodic ataxia,
XX autosomal dominant myokymia, stroke, Parkinson's disease, Alzheimer's
XX disease, non-insulin dependent diabetes mellitus, asthma, hypertension
XX and seizure (NOV4), enamel defects, such as amelogenesis imperfecta and
XX disorders involving enamel defects, including hypoplasia and
XX hypomineralisation (NOV5-7), paraneoplastic neurological disorders, e.g.
XX paraneoplastic limbic of brain-stem encephalitis occurring during
XX testicular cancer, diabetes, reproductive health, metabolic and autoimmune
XX disorders, gastrointestinal disorders, immune disorders and autoimmune
XX diseases, respiratory disorders, bone disorders, musculoskeletal
XX disorders, leukaemia/lymphoma and tissue/cell growth regulation disorders
XX (NOV8), lesional psoriatic skin (NOV9-10) and atherosclerosis, abdominal
XX aortic aneurysm and neurological disorders (NOV11). NOVX polypeptide is
XX also useful for identifying an agent that binds to it and a cell
XX expressing NOVX polypeptide is useful for identifying a therapeutic agent

CC for use in treatment of a NOVX related pathology. The antibodies and a
 CC polypeptide having 95% sequence identity to NOVX polypeptide are useful
 CC for treating a pathological state in a mammal. The present sequence
 CC represents NOV8, a possible neuronal antigen-like protein

XX Sequence 351 AA;

Query Match 35.4%; Score 271.5; DB 4; Length 351;
 Best Local Similarity 44.6%; Pred. No. 6.4e-21;
 Matches 58; Conservative 32; Mismatches 29; Indels 11; Gaps 3;
 QY 1 DLMHIVQADNPISVVEECLEAFKQVFGSLRRRTAQVRLKPYQEGEKVSAYVRLRLETL 60
 Db 216 DVIRVLKINNPLITVDECLQALEEVFGVTDNPRLQVKYLTYYQDEKLSAYVRLRLEPL 275
 QY 61 LRRRAVEKRAIPRRITADQVRLEQVWAGA---TLNQMLWCRLRELKDQGGPPSPFLELMKVIR 117
 Db 276 LQKLVQVGAERDAVNQARLDQVIAGAVHKTIRREL-----NLPEDGAPGFLQLLVLIK 330
 QY 118 E---EEEEEA 124
 Db 331 DYEAEEEEEA 340

RESULT 15

AAB94854
 ID AAB94854 standard; protein: 237 AA.

AC AAB94854;

XX 26-JUN-2001 (first entry)

XX Human protein sequence SEQ ID NO:16040.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-00116126.

XX 29-JUL-1999; 99JP-00248036.

XX 27-AUG-1999; 99JP-00300253.

XX 11-JAN-2000; 2000JP-00118776.

XX 02-MAY-2000; 2000JP-00183767.

XX 09-JUN-2000; 2000JP-00241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX Claim 8; SEQ ID NO 16040; 2537pp + Sequence Listing; English.

CC The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention

XX Sequence 237 AA;

Query Match 34.8%; Score 266.5; DB 4; Length 237;
 Best Local Similarity 43.8%; Pred. No. 1.3e-20;
 Matches 57; Conservative 33; Mismatches 29; Indels 11; Gaps 3;

QY 1 DLMHIVQADNPISVVEECLEAFKQVFGSLRRRTAQVRLKPYQEGEKVSAYVRLRLETL 60

Db 102 DVIRVLKINNPLITVDECLQALEEVFGVADNPRLQVKYLTTHQDEKLSAYVRLRLEPL 161

QY 61 LRRRAVEKRAIPRRITADQVRLEQVWAGA---TLNQMLWCRLRELKDQGGPPSPFLELMKVIR 117

Db 162 LQKLVQVGAERDAVNQARLDQVIAGAVHKTIRREL-----NLPEDGAPGFLQLLVLIK 216

QY 118 E---EEEEEA 124

Db 217 DYEAEEEEEA 226

Search completed: September 27, 2004, 17:08:22

Job time : 29.0768 secs

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